

From: Fredman, Jeffrey  
 Sent: Tuesday, January 25, 2005 6:06 AM  
 To: STIC-Biotech/ChemLib  
 Cc: Schultz, James  
 Subject: FW: RUSH sequence search 09/828,870

PLEASE RUSH.

I Approve.

Jeff Fredman

-----Original Message-----

From: Schultz, James  
 Sent: Monday, January 24, 2005 5:16 PM  
 To: Fredman, Jeffrey  
 Subject: RUSH sequence search 09/828,870

RECEIVED  
 (STIC)  
 2005 JAN 25 PM  
 2005 JAN 25 PM

Hi Jeff,

If you approve the following rush request, could you please forward this to STIC-biotech? This case was a transfer for which I thought the sequence searches had been ordered. There are two sequences because they have been disclosed as useful together.

Thanks,  
 Doug Schultz

STIC searchers,

Could you please run RUSH standard amino acid sequence searches against both SEQ ID NOS:36 and 39 (both 20 aa long) in the above entitled case?

Thanks,  
 Doug Schultz

James Douglas Schultz, PhD  
 AU 1635 (Biotechnology)  
 Patent Examiner  
 United States Patent and Trademark Office  
 (Office) REM 2D18  
 (Mail) REM 2C18  
 (571) 272-0763

\*\*\*\*\*

STAFF USE ONLY

Searcher: *Jan*  
 Searcher Phone: 2-2504  
 Date Searcher Picked up: 1/25/05  
 Date Completed: 1/26/05  
 Searcher Prep/Rev. Time: 10  
 Online Time: 115

\*\*\*\*\*

Type of Search  
 NA Sequence: #  
 AA Sequence: #   
 Structure: #  
 Bibliographic:  
 Litigation:  
 Patent Family:  
 Other:

\*\*\*\*\*

Vendors and cost where applicable  
 STN: \_\_\_\_\_  
 DIALOG: \_\_\_\_\_  
 QUESTEL/ORBIT: \_\_\_\_\_  
 LEXIS/NEXIS: \_\_\_\_\_  
 SEQUENCE SYSTEM:   
 WWW/Internet: \_\_\_\_\_  
 Other(Specify): \_\_\_\_\_

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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.	Run on: January 26, 2005, 00:05:26 ; Search time 169 Seconds (without alignments) 42.453 Million cell updates/sec	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 4 summaries	RESULT 1 AAU77891 ID AAU77891 standard; peptide: 20 AA. XX AC AAU77891; XX DT 05-JUN-2002 (first entry) XX DB Bak GD binding domain derived Peptide #2. XX KW GD domain; apoptosis; interaction with Bcl-XL; cell killing function; KW cell death regulatory molecule; autoimmune disease; cancer; mutant; KW mutant. XX Unidentified. OS Synthetic. XX PN US6221615-B1. XX PD 24-APR-2001. XX 25-JAN-1999; 99US-002216385. XX PR 12-MAY-1995; 95US-00410391. PR 08-AUG-1997; 97US-00938597. XX (APOPO-) APOPTOSIS TECHNOLOGY INC. XX PI Chittenden TD, Lutz RJ; XX DR WPI; 2002-234950/29. XX Identifying agents (e.g. modulators of apoptosis) capable of modulating GD domain mediated heterodimerization or homodimerization comprises carrying out a heterodimerization or homodimerization assay. XX Example: Col 22: 37PP; English.
Copyright (c) 1993 - 2005 Compugen Ltd.			
OM protein - protein search, using sw model			
Run on: Title: US-09-828-870-36 Perfect score: 102 Sequence: 1 TMQGVGRQLAIIGDINRY 20	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	Searched: 2002273 seqs, 358729299 residues	Total number of hits satisfying chosen parameters: 2002273
Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Minimum Match 0% Maximum Match 100%	Listing first 4 summaries	
Database : A_Geneseq_23Sep04:*			
1: GeneseqP1980s:*			
2: GeneseqP1990s:*			
3: GeneseqP2000s:*			
4: GeneseqP2001s:*			
5: GeneseqP2002s:*			
6: GeneseqP2003s:*			
7: GeneseqP2003s:*			
8: GeneseqP2004s:*			
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			
		SUMMARIES	
Result No.	Score	Query Match Length DB ID	Description
1	102	100.0 20 ADK14723	Aau77891 Bak GD bi Adk14723 Bcl-2 rel Aay96322 Mammalian
2	102	100.0 20 8 ADK14723	Aab70372 BAK BH3 C Aab37004 Bcl2 poly Aaw06294 GD domain
3	102	100.0 26 3 AAY96322	Aau77877 Bak GD do Adk14689 BCL-2 rel Aar77877 Human Cdn Aar77876 Human Cdn
4	102	100.0 26 4 AAB70372	Aau7789 Bak GD do Adk14689 BCL-2 rel Aar77877 Human Cdn Aar77876 Human Cdn
5	102	100.0 27 3 AAB37004	Aau7789 Bak GD do Adk14689 BCL-2 rel Aar77877 Human Cdn Aar77876 Human Cdn
6	102	100.0 28 3 AAW06294	Aau7789 Bak GD do Adk14689 BCL-2 rel Aar77877 Human Cdn Aar77876 Human Cdn
7	102	100.0 28 3 AAR77877	Aau7789 Bak GD do Adk14689 BCL-2 rel Aar77877 Human Cdn Aar77876 Human Cdn
8	102	100.0 28 8 ADK14689	Aau7789 Bak GD do Adk14689 BCL-2 rel Aar77877 Human Cdn Aar77876 Human Cdn
9	102	100.0 28 8 ADK14705	Aau7789 Bak GD do Adk14705 BCL-2 rel Aar77877 Human Cdn Aar77876 Human Cdn
10	102	100.0 36 5 AAU77891	Aau7789 Bak GD do Adk14701 Bak GD do Aar77879 Human Cdn Aar77876 Human Cdn
11	102	100.0 36 8 ADK14701	Aau7789 Bak GD do Adk14701 Bak GD do Aar77879 Human Cdn Aar77876 Human Cdn
12	102	100.0 152 2 AAR77879	Aau7789 Bak GD do Adk14701 Bak GD do Aar77879 Human Cdn Aar77876 Human Cdn
13	102	100.0 211 2 AAR77877	Aau7789 Bak GD do Adk14701 Bak GD do Aar77877 Human Cdn Aar77876 Human Cdn
14	102	100.0 211 2 AAR77877	Aau7789 Bak GD do Adk14701 Bak GD do Aar77877 Human Cdn Aar77876 Human Cdn
15	102	100.0 211 2 AAR81451	Aau7789 Bak GD do Adk14701 Bak GD do Aar77877 Human Cdn Aar77876 Human Cdn
16	102	100.0 211 2 AAW03668	Aaw03668 Bak-2 pro Aaw03669 Bak-2 pro Aaw72534 Bak polyP
17	102	100.0 211 2 AAW03669	Aaw03669 Bak-2 pro Aaw72534 Bak polyP
18	102	100.0 211 2 AAW03669	Aaw03669 Bak-2 pro Aaw72534 Bak polyP
19	102	100.0 211 2 AAY05433	Aay05433 Human BAK Abb82374 Human BAK
20	102	100.0 211 6 AEE37655	Aee37655 Bcl2 rela Aee37655 Bcl2 rela
21	102	100.0 211 6 AEE37655	Aee37655 Bcl2 rela Aee37655 Bcl2 rela
22	102	100.0 211 6 AB47397	AB47397 Breast ca Add93300 Human pro Add60830 Human Bak
23	102	100.0 211 7 ADD93300	AB47397 Breast ca Add93300 Human pro Add60830 Human Bak
24	102	100.0 211 7 ADD60830	AB47397 Breast ca Add93300 Human pro Add60830 Human Bak
25	100.0	211 8 AAM52299	Aam52299 Miniature
		ALIGNMENTS	

CC apoptosis. The present sequence representing a Bak GD binding domain derived peptide is used in the methods of the present invention

XX SQ Sequence 20 AA;

Query Match 100.0%; Score 102; DB 5; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.8e-10;

Matches 20; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

Qy 1 TMGQVRQLAIGDDINRY 20

Db 1 TMGQVRQLAIGDDINRY 20

RESULT 2

ADK14723 ID ADK14723 standard; peptide; 20 AA.

XX AC ADK14723;

XX DT 03-JUN-2004 (first entry)

DE BCL-2 related gene Bak residues 70-89 seqid 36.

XX KW anti-HIV; dermatological; immunosuppressive; antiinflammatory;

KW antirheumatic; antiarthritic; GD domain peptide; apoptosis;

KW protein domain; GD domain; bcl-2 related gene; Bak; cell death;

KW immunoreactive protein; degenerative disorder;

KW cell proliferation disorder; cell death disorder; autoimmune disease;

KW systemic lupus erythematosus; SLE; rheumatoid arthritis;

KW acquired immunodeficiency syndrome; AIDS.

XX OS Unidentified.

XX PN US2004054129-A1.

XX PD 18-MAR-2004.

XX PP 10-APR-2001; 2001US-00828870.

XX PR 12-MAY-1995; 95US-00440391.

PR 08-AUG-1997; 97US-00908597.

PR 25-JAN-1999; 99US-00236385.

XX PA (APOPTOSIS TECHNOLOGY INC.

XX PI Chittenden TD, Lutz RJ;

XX WPI; 2004-247780/23.

XX Novel isolated and purified peptide comprising GD domain, useful for

PT treating degenerative disease e.g., rheumatoid arthritis.

XX Example; SEQ ID NO 36; 38pp; English.

CC The invention describes an isolated and purified peptide (I) comprising

CC unrecognised protein domain (GD domain) isolated from the bcl-2 related

CC gene Bak that can induce cell death. (I) is useful for identifying an

CC agent capable of modulating GD domain radiated heterodimerisation or

CC homodimerisation. (IV) is useful for screening a cDNA expression library

CC for clones comprising DNA inserts encoding immunocrossreactive proteins

CC (claimed). An anti-(I)-antibody, its mimetics, functional

CC equivalents and/or hybrids or its mutants, and a vector comprising a

CC polynucleotide encoding (I) are useful as agents for treating

CC degenerative disorders including disorders having inappropriate cell

CC proliferation or inappropriate cell death. The agents are also useful for

CC treating disorders in which a cell is present and/or persists in an

CC inappropriate location, and autoimmune disease such as systemic lupus

CC erythematosus (SLE) and rheumatoid arthritis. The degenerative disorder

CC include acquired immunodeficiency syndrome (AIDS). This is the amino acid

CC sequence of Bak residues 70-89, a variant of the GD domain uniquely

CC required for Bak's cell killing function.

SQ Sequence 20 AA;

Query Match 100.0%; Score 102; DB 8; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.8e-10;

Matches 20; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

Qy 1 TMGQVRQLAIGDDINRY 20

Db 1 TMGQVRQLAIGDDINRY 20

RESULT 3  
AY95322 ID AY95322 standard; peptide; 26 AA.

XX AC AY95322;

XX DT 17-AUG-2000 (first entry)

XX DE Mammalian Bak Bcl-2 homology domain 3 domain.

XX KW Mammal; apoptosis; cell death; BBC3; apoptosis promotion; Bak;

KW apoptosis inhibition; malignant cell; autoimmune disease.

XX Mammalia.

OS XX

PN WO200026228-A1.

XX PD 11-MAY-2000.

XX PP 28-OCT-1999; 99WO-US025285.

XX PR 02-NOV-1998; 98US-00184168.

XX DR WPI; 2000-365560/31.

XX PA (CLON- CLONTECH LAB INC.

XX PI Zhu L, Yin X, Chittenden T;

XX XX Disclosure; Fig 4; 47pp; English.

PS XX

CC The present sequence is the mammalian Bak Bcl-2 homology domain 3 (BH3)

CC domain, which was used in a sequence alignment with the same domain of a

CC putative version of the mammalian apoptosis regulator BBC3, which was

CC designated BBC3-ORF2. The BBC3 protein, nucleic acids

CC and antibodies are

CC suitable for use in promoting cell death or for preventing apoptosis in

CC malignant cells and those causing autoimmune diseases.

XX SQ Sequence 26 AA;

Query Match 100.0%; Score 102; DB 3; Length 26;

Best Local Similarity 100.0%; Pred. No. 2.5e-10;

Matches 20; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

Qy 1 TMGQVRQLAIGDDINRY 20

Db 1 TMGQVRQLAIGDDINRY 20

RESULT 4  
AAB70372 ID AAB70372 standard; peptide; 26 AA.

XX AC AAB70372;

XX DT 02-MAY-2001 (first entry)

XX DB BAK BH3 consensus peptide sequence SEQ ID NO:5.

Bcl-XL/Bcl-2 associated cell death regulator; Bcl-XL mutant; apoptosis; immunomodulant; neuroprotective; nootropic; anti-ischaemic; vulnerability; cytostatic; antiviral; antiarthritic; antiinflammatory; wound healing; immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer; immunodeficiency disease; neurodegenerative disease; viral infection; ischaemic cell death; reperfusion cell death; arthritis; infertility; lymphoproliferative condition; inflammation; autoimmune disease.

Unidentified.

WO200108888-A1.

15-FEB-2001.

30-MAY-2000; 20000WO-US011864.

28-MAY-1999; 99US-0136793P.

(APOP-) APOPTOSIS TECHNOLOGY INC.

Zhou X;

WPI; 2001-138734/14.

New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide, useful for screening for candidate compounds which induce or inhibit apoptosis, comprises amino acid substitutions at Ser118, Ser155 or Ser113.

Example 2: Fig 3a; 157pp; English.

The present invention describes an isolated or synthetic polypeptide (I) comprising a less than full length amino acid sequence of a mutant Bcl-2-associated cell death regulator polypeptide (BAD) or its fragment, which contains amino acid substitutions at Ser18 of a human BAD, Ser155 of a murine BAD or Ser118 of a murine BAD (shorter murine BAD) (I) has immunostimulant, neuroprotective, antihistocytic, antiischaemic, vulnerary, cytostatic, antiviral, antiarthritic, antiinflammatory and immunosuppressive activities, and can be used as an apoptosis inducer or inhibitor. BAD polypeptides and nucleotides can be used for screening candidate compounds and drugs for activity that promote cell survival or apoptosis. Other uses include inducing or inhibiting apoptosis in a cell. Candidate compounds identified and (mutant) BAD polypeptides are useful in treating neurodegenerative diseases, neurodegenerative diseases, ischaemic cell death, reperfusion cell death, wound healing, cancer, viral infections, lymphoproliferative conditions, arthritis, infertility, inflammation and autoimmune diseases. The present sequence represents a Bcl-family member (HR31) domain consensus sequence which is used in an example from the

Sequence 26 AA:		Sequence 26 AA:	
Query Match	100.0%	Score 102;	DB 4;
Best Local Similarity	100.0%	Pred. No.	2.5e-10;
Marches 20.	Conservative	No. Mismatches	0.
		Random	0.
		No. Cans	0.

RESULT 6					
AAW06294      AAW06294 standard; peptide; 28 AA.					
Qy	1	TMGQVGRQLAIIGDDINRY	20		
Db	4	TMGQVGRQLAIIGDDINRY	23		
		XX	XX		
		AC	AC		
		AAW06294;	AAW06294;		
		DT	DT	29-JUL-1997	(first entry)

**Cytostatic;** neuroprotective; anti-HIV; virucide; cerebroprotective; cardiot; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma; melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS; stroke; myocardial infarction.

**KW** KW Homo sapiens.

**KW** KW XX

**KW** KW OS

**KW** KW PN

WO20005926-A1.

XX GD domain region for Bak amino acid residues 67-94.  
 DE XX PF 25-JAN-1999; 99US-00236385.  
 KW XX PR 12-MAY-1995; 95US-00440391.  
 XX PR 08-AUG-1997; 97US-00988597.  
 OS XX PA (APOP-) APOPTOSIS TECHNOLOGY INC.  
 PN XX  
 PN WO9635951-A1.  
 XX PI Chittenden TD, Lutz RJ;  
 XX DR WPI: 2002-234450/29.  
 XX DR N-PSDB; ABK11177.  
 XX PT Identifying agents (e.g. modulators of apoptosis) capable of modulating  
 XX PT GD domain mediated heterodimerization or homodimerization comprises  
 XX PT carrying out a heterodimerization or homodimerization assay.  
 XX PA (IMMU-) IMMUNOSEN INC.  
 XX PS Claim 1; Fig 8A; 37pp; English.  
 XX CC The present invention relates to novel peptides, designated GD domains, which are capable of modulating apoptosis. The GD domains are essential for Bak's interaction with Bcl-XL, and to Bak's cell killing function.  
 XX CC The GD domains mediate key protein/protein interactions with multiple cell death regulatory molecules. Also described are methods of identifying agonists or antagonists of GD domains. The methods are useful for identifying agents capable of modulating GD domain mediated heterodimerisation or homodimerisation. The methods are particularly useful in drug screening and design, e.g. for identifying agents for treating autoimmune disease or cancer, or for identifying modulators of apoptosis. The present sequence represents a GD domain region  
 XX SQ Sequence 28 AA;  
 XX Query Match 100.0%; Score 102; DB 5; Length 28;  
 XX Best Local Similarity 100.0%; Pred. No. 2.7e-10;  
 XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 Qy 1 TMGQYGRQLAIIGDDINRY 20  
 Db 4 TMGQYGRQLAIIGDDINRY 23  
 XX Sequence 28 AA;  
 XX RESULT 8  
 ID ADK14689 standard; peptide; 28 AA.  
 XX ID ADK14689  
 XX AC ADK14689;  
 XX AC ADK14689;  
 XX DT 03-JUN-2004 (first entry)  
 XX DE BC1-2 related gene Bak residues 67-94 seqid 2.  
 XX XX  
 XX KW anti-HIV; dermatological; immunosuppressive; antiinflammatory;  
 XX KW anti-rheumatic; antiarthritic; GD domain peptide; apoptosis;  
 XX KW protein domain; GD domain; bcl-2 related gene; Bak; cell death;  
 XX KW immunocrossreactive protein; degenerative disorder;  
 XX KW cell proliferation disorder; cell death disorder; autoimmune disease;  
 XX KW systemic lupus erythematosus; SLE; rheumatoid arthritis;  
 XX KW acquired immunodeficiency syndrome; AIDS.  
 XX OS Unidentified.  
 XX PN US20040541129-A1.  
 XX PD 18-MAR-2004.  
 XX PP 10-APR-2001; 2001US-00828870.  
 XX PR 12-MAY-1995; 95US-00440391.  
 XX PR 08-AUG-1997; 97US-00988597.  
 XX PR 25-JAN-1999; 99US-00236385.  
 XX PA (APOP-) APOPTOSIS TECHNOLOGY INC.  
 XX  
 XX AC AAU77877;  
 XX DT 05-JUN-2002 (first entry)  
 XX DE Bak GD domain region #2 for modulating apoptosis.  
 XX KW GD domain; apoptosis; interaction with Bcl-XL; cell killing function;  
 XX KW bak; cell death regulatory molecule; autoimmune disease; cancer.  
 OS Unidentified.  
 XX PN US6221615-B1.  
 XX PD 24-APR-2001.

PI Chittenden TD, Lutz RJ;  
 XX WPI: 2004-247780/23.  
 PT Novel isolated and purified peptide comprising GD domain, useful for  
 PT treating degenerative disease e.g., rheumatoid arthritis.  
 XX  
 PS Claim 2; SEQ ID NO 2; 38pp; English.

XX The invention describes an isolated and purified peptide (I) comprising a GD domain (GP domain) isolated from the bcl-2 related gene Bak that can induce cell death. (I) is useful for identifying an agent capable of modulating GD domain radiated heterodimerisation or homodimerisation. (IV) is useful for screening a cDNA expression library for clones comprising DNA inserts encoding immunocrossreactive proteins for clones comprising DNA inserts encoding immunocrossreactive proteins (claimed). An anti-(I)-antibody, its mimetics, fragments, functional equivalents and/or hybrids or its mutants, and a vector comprising a polynucleotide encoding (I) are useful as agents for treating degenerative disorders including disorders having inappropriate cell proliferation or inappropriate cell death. The agents are also useful for treating disorders including disorders having inappropriate cell proliferation or inappropriate cell death. The agents are also useful for treating disorders in which a cell is present and/or persists in an inappropriate location, and autoimmune disease such as systemic lupus erythematosus (SLE) and rheumatoid arthritis. The degenerative disorder include acquired immunodeficiency syndrome (AIDS). This is the amino acid sequence of Bak residues 67-94, uniquely required for Bak's cell killing function.  
 XX  
 SQ Sequence 28 AA;  
 Query Match 100.0%; Score 102; DB 8; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-10;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 TMGQVRQLAITGDDINRY 20  
 Db 4 TMGQVRQLAITGDDINRY 23

RESULT 9  
 ADK14705  
 ID ADK14705 standard; peptide; 28 AA.  
 XX  
 AC ADK14705;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX BC1-2 related gene Bak residues 67-94 seqid 18.  
 XX anti-HIV; dermatological; immunosuppressive; antiinflammatory;  
 KW antirheumatic; antirheumatic; GD domain peptide; apoptosis;  
 KW protein domain; GD domain; bcl-2 related gene; Bak; cell death;  
 KW immunocrossreactive protein; degenerative disorder; Bak; cell death;  
 KW cell proliferation disorder; cell death disorder; autoimmune disease;  
 KW systemic lupus erythematosus; SLE; rheumatoid arthritis;  
 KW acquired immunodeficiency syndrome; AIDS.  
 XX Unidentified.  
 XX  
 PN US2004054129-A1.  
 XX  
 PD 18-MAR-2004.  
 XX  
 PP 10-APR-2001; 2001US-00828870.  
 XX  
 PR 12-MAY-1995; 95US-00440391.  
 PR 08-AUG-1997; 97US-00908597.  
 PR 25-JAN-1999; 99US-00236385.  
 XX  
 PA (APOP-) APOPTOSIS TECHNOLOGY INC.  
 XX  
 PI Chittenden TD, Lutz RJ;  
 XX  
 DR 2002-234950/29.  
 PR 08-AUG-1997; 97US-0098597.  
 XX  
 PA (APOP-) APOPTOSIS TECHNOLOGY INC.  
 XX  
 PI Chittenden TD, Lutz RJ;  
 XX  
 WPI: 2004-247780/23.

DR N-PSDB; ADK14704.  
 XX PT Novel isolated and purified peptide comprising GD domain, useful for  
 PT treating degenerative disease e.g., rheumatoid arthritis.  
 XX  
 PS Disclosure; SEQ ID NO 18; 38pp; English.

XX The invention describes an isolated and purified peptide (I) comprising an unrecognised protein domain (GD domain) isolated from the bcl-2 related gene Bak that can induce cell death. (I) is useful for identifying an agent capable of modulating GD domain radiated heterodimerisation or homodimerisation. (IV) is useful for screening a cDNA expression library for clones comprising DNA inserts encoding immunocrossreactive proteins (claimed). An anti-(I)-antibody, its mimetics, fragments, functional equivalents and/or hybrids or its mutants, and a vector comprising a polynucleotide encoding (I) are useful as agents for treating degenerative disorders including disorders having inappropriate cell proliferation or inappropriate cell death. The agents are also useful for treating disorders in which a cell is present and/or persists in an inappropriate location, and autoimmune disease such as systemic lupus erythematosus (SLE) and rheumatoid arthritis. The degenerative disorder include acquired immunodeficiency syndrome (AIDS). This is the amino acid sequence of Bak residues 67-94, uniquely required for Bak's cell killing function.  
 XX  
 SQ Sequence 28 AA;  
 Query Match 100.0%; Score 102; DB 8; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-10;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 TMGQVRQLAITGDDINRY 20  
 Db 4 TMGQVRQLAITGDDINRY 23

RESULT 10  
 AAU77889  
 ID AAU77889 standard; peptide; 36 AA.  
 XX  
 AC AAU77889;  
 XX  
 DT 05-JUN-2002 (first entry)  
 XX Bak GD domain used to identify homologous regions in Bax and Bip1a.  
 DE Bak GD domain used to identify homologous regions in Bax and Bip1a.  
 XX  
 KW GD domain; apoptosis; interaction with Bcl-XL; cell killing function;  
 KW bak; cell death regulatory molecule; autoimmune disease; cancer; bax;  
 KW bip1a.  
 XX  
 OS Unidentified.  
 XX  
 PN US6221615-B1.  
 XX  
 PD 24-APR-2001.  
 XX  
 PP 25-JAN-1999; 99US-00236385.  
 XX  
 PR 12-MAY-1995; 95US-00440391.  
 PR 08-AUG-1997; 97US-0098597.  
 XX  
 PA (APOP-) APOPTOSIS TECHNOLOGY INC.  
 XX  
 PI Chittenden TD, Lutz RJ;  
 XX  
 DR 2002-234950/29.  
 PR 08-AUG-1997; 97US-0098597.  
 XX  
 PA (APOP-) APOPTOSIS TECHNOLOGY INC.  
 XX  
 PI Chittenden TD, Lutz RJ;  
 XX  
 WPI: 2004-247780/23.

XX  
 PT Identifying agents (e.g. modulators of apoptosis) capable of modulating GD domain mediated heterodimerization or homodimerization comprises PT carrying out a heterodimerization or homodimerization assay.  
 XX  
 PS Example; Fig 5; 37pp; English.  
 XX

The present invention relates to novel peptides, designated GD domains, which are capable of modulating apoptosis. The GD domains are essential for Bak's interaction with Bcl-XL, and to Bak's cell killing function. The GD domains mediate key protein/protein interactions with multiple cell death regulatory molecules. Also described are methods of identifying agonists or antagonists of GD domains. The methods are useful for identifying agents capable of modulating GD domain mediated heterodimerisation or homodimerisation. The methods are particularly useful in drug screening and design, e.g. for identifying modulators of treating autoimmune disease or cancer, or for identifying modulators of apoptosis. The present sequence representing a Bak GD domain is used to identify homologous regions in Bp1a and Bak

Sequence 36 AA;

Query Match 100.0%; Score 102; DB 5; Length 36;  
Best Local Similarity 100.0%; Pred. No. 3 6e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SEQ 1 TMGQVERQRLAIIQGDIDNRY 20  
6 TMGQVERQRLAIIQGDIDNRY 25

Sequence 36 AA;

Query Match 100.0%; Score 102; DB 5; Length 36;  
Best Local Similarity 100.0%; Pred. No. 3 6e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SEQ 1 TMGQVERQRLAIIQGDIDNRY 20  
6 TMGQVERQRLAIIQGDIDNRY 25

Sequence 36 AA;

Query Match 100.0%; Score 102; DB 5; Length 36;  
Best Local Similarity 100.0%; Pred. No. 3 6e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SEQ 1 TMGQVERQRLAIIQGDIDNRY 20  
6 TMGQVERQRLAIIQGDIDNRY 25

Sequence 36 AA;

Query Match 100.0%; Score 102; DB 5; Length 36;  
Best Local Similarity 100.0%; Pred. No. 3 6e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SEQ 1 TMGQVERQRLAIIQGDIDNRY 20  
6 TMGQVERQRLAIIQGDIDNRY 25

Sequence 36 AA;

Query Match 100.0%; Score 102; DB 5; Length 36;  
Best Local Similarity 100.0%; Pred. No. 3 6e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SEQ 1 TMGQVERQRLAIIQGDIDNRY 20  
6 TMGQVERQRLAIIQGDIDNRY 25

Sequence 36 AA;

Query Match 100.0%; Score 102; DB 5; Length 36;  
Best Local Similarity 100.0%; Pred. No. 3 6e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SEQ 1 TMGQVERQRLAIIQGDIDNRY 20  
6 TMGQVERQRLAIIQGDIDNRY 25

Sequence 36 AA;

Query Match 100.0%; Score 102; DB 5; Length 36;  
Best Local Similarity 100.0%; Pred. No. 3 6e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SEQ 1 TMGQVERQRLAIIQGDIDNRY 20  
6 TMGQVERQRLAIIQGDIDNRY 25

Sequence 36 AA;

Query Match 100.0%; Score 102; DB 5; Length 36;  
Best Local Similarity 100.0%; Pred. No. 3 6e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SEQ 1 TMGQVERQRLAIIQGDIDNRY 20  
6 TMGQVERQRLAIIQGDIDNRY 25

Sequence 36 AA;

Query Match 100.0%; Score 102; DB 5; Length 36;  
Best Local Similarity 100.0%; Pred. No. 3 6e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SEQ 1 TMGQVERQRLAIIQGDIDNRY 20  
6 TMGQVERQRLAIIQGDIDNRY 25

Sequence 36 AA;

Query Match 100.0%; Score 102; DB 5; Length 36;  
Best Local Similarity 100.0%; Pred. No. 3 6e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SEQ 1 TMGQVERQRLAIIQGDIDNRY 20  
6 TMGQVERQRLAIIQGDIDNRY 25

CC polynucleotide encoding (I) are useful as agents for treating degenerative disorders including disorders having inappropriate cell proliferation or inappropriate cell death. The agents are also useful for treating disorders in which a cell is present and/or persists in an inappropriate location, and autoimmune disease such as systemic lupus erythematosus (SLE) and rheumatoid arthritis. The degenerative disorder include acquired immunodeficiency syndrome (AIDS). This is the amino acid sequence of the Bak GD domain.

XX



XX	WPI; 1996-139648/14.	CC	disruption of the interaction, e.g. by co-precipitation, protein
DR	N-PSDB; AAT17375.	CC	interactive trapping or ELISA. Interaction of Bak and viral proteins
XX	New isolated human Bcl- $\gamma$ protein - used to develop prods. for treating	CC	allows viral replication or latency in the absence of apoptosis.
PT	PT	CC	Compounds which inhibit the interaction may be used as virucide,
PT	disorders characterised by inappropriate cell proliferation or cell	CC	antitumour or diagnostic agents
PT	death.	XX	
XX	Sequence 211 AA;	SQ	Sequence 211 AA;
PS	Claim 3; Fig 4; 100pp; English.	Query Match	100.0%; Score 102; DB 2;
XX	Bcl- $\gamma$ protein (AARB1451) is a member of the Bcl-2 family and can induce	Best Local Similarity	100.0%; Pred. No. 2 8e-09;
CC	apoptosis in cells and function as a negative regulator of Bcl-2	Matches	0; Mismatches 0; Indels 0; Gaps 0;
CC	function. Bcl- $\gamma$ mRNA was detected in all human tumour cell lines examined	Qy	1 TMGQVGRQLAIGDDINRY 20
CC	and is also widely expressed in primary human tissues. It can be obcd. by	Db	70 TMGQVGRQLAIGDDINRY 89
CC	expression of a full-length cDNA clone (AAT17375) in pref. mammalian host		
CC	cells. Bcl- $\gamma$ can be used to develop prods. for treating disorders		
CC	associated with inappropriate cell proliferation or cell death, and to	RESULT 17	
CC	raise antibodies used for the diagnosis or monitoring of such disorders	AAW03669	
XX	Sequence 211 AA;	ID	AAW03669 standard; protein; 211 AA.
XX	Query Match	100.0%; Score 102; DB 2;	
XX	Best Local Similarity	100.0%; Pred. No. 2.8e-09;	
XX	Matches	0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 TMGQVGRQLAIGDDINRY 20	XX	
Db	70 TMGQVGRQLAIGDDINRY 89	XX	
		XX	Bak-2 protein.
		XX	Human; Bak-2; apoptosis; latency; virus replication; Epstein-Barr virus;
		XX	BHRF1; fusion protein; epitope tag; drug screening; co-precipitation;
		XX	ELISA; immunoassay; antibody; protein interactive trapping; virucide;
		XX	antitumour; diagnostic.
		OS	Homo sapiens.
		XX	
		AC	W09633416-A1.
		XX	
		PN	
		XX	
		PD	24-OCT-1996.
		XX	
		PP	19-APR-1996;
		XX	96WO-US005639.
		PR	20-APR-1995;
		XX	95US-00426529.
		PA	(LXR-B-) LXR BIOTECHNOLOGY INC.
		XX	
		PI	Barr PJ, Kiefer MC;
		XX	
		WPI	1996-485886/48.
		DR	
		N-PSDB	; AAT42139.
		XX	Screening for anti-viral agents - by detecting the ability of an agent to
		PT	disrupt the interaction of a Bak protein and a viral protein.
		XX	
		PS	Disclosure; Fig 2; 24pp; English.
		XX	
		CC	This Bak-2 protein sequence represents a bcl-1 homologue which interacts
		CC	with Epstein-Barr virus (EBV) early lytic cycle BHRF1 protein, and is
		CC	capable of modulating apoptosis. The protein may be used in complete or
		CC	partial form, or as an epitope tag fusion protein in a new viricide drug
		CC	screening method, which involves combination of Bak-2 protein and a viral
		CC	protein (e.g. EBV BHRF1), exposure to a test compound, and monitoring for
		CC	disruption of the interaction, e.g. by co-precipitation, protein
		CC	interactive trapping or ELISA. Interaction of Bak-2 and viral proteins
		CC	allows viral replication or latency in the absence of apoptosis.
		CC	Compounds which inhibit the interaction may be used as virucide,
		CC	antitumour or diagnostic agents.
		XX	
		SQ	Sequence 211 AA;
		Query Match	100.0%; Score 102; DB 2;
		Best Local Similarity	100.0%; Pred. No. 2.8e-09;
		Matches	0; Mismatches 0; Indels 0; Gaps 0;
		Qy	1 TMGQVGRQLAIGDDINRY 20

Db	70 TMGQVGRQLAIGDDINRY 89	Qy	1 TMGQVGRQLAIGDDINRY 20
RESULT 18		Db	70 TMGQVGRQLAIGDDINRY 89
AAW79534	standard; peptide; 211 AA.	AY05433	
ID AAW79534		ID AAY05433	standard; peptide; 211 AA.
XX		XX	
AC AAW79534;		AC AAY05433;	
XX		XX	
DT 11-JAN-1999	(first entry)	DT 02-JUL-1999	(first entry)
XX		XX	
DB Bak polypeptide.		DE Human BAK protein sequence.	
XX		XX	
KW Bak; bak binding protein; BBP; BBPBD-1; BbPBD-2; Bcl-2; apoptosis; cell death; cancer; lymphoma; neurodegeneration; heart disease; cell proliferation; infection; human; therapy; diagnosis.		KW BH3 domain; cell death agonist; bcl homology domain; Bcl-2 family; apoptosis promoter; cancer cell; virus infected cell; inflammation; autoantibody producing cell; cancer; lymphoproliferative condition; arthritis; autoimmune disease; therapy.	
XX		XX	
OS Homo sapiens.		KW	
XX		XX	
PH	Location/Qualifiers	XX	
PT Peptide	103 . 126	PN WO9916787-A1.	
PT	/label= "BBPBD-1"	XX	
PT	/note= "Claim 36"	PD 08-APR-1999.	
PT	138 . 156	XX	
PT	/label= BBPBD-2	PP 22-SEP-1998;	
PT	/note= "Claim 62"	XX	98WO-US019765.
XX		XX	
PN WO9841626-A1.		PR 26-SEP-1997;	97US-0060133P.
XX		PR 07-OCT-1997;	
PD 24-SEP-1998.		XX	97US-00946039.
XX		XX	
PP 03-MAR-1998;	98WO-US004079.	(UNIW ) UNIV WASHINGTON.	
XX		PA	
PR 20-MAR-1997;	97US-0041328P.	PI Kornmeyer SJ;	
PR 09-JAN-1996;	98US-0071037P.	XX	
XX		DR WPI; 1999-255058/21.	
PA (LXRB-) LXR BIOTECHNOLOGY INC.		XX	
XX		PT PT	
PI Kiefer MC, Fitzpatrick PA, Gibson HL, Barr PJ;		XX	
XX		PS Disclosure; Fig 21b; 10pp; English.	
DR WPI; 1998-521220/44.		XX	
DR N-PSDB; AA961498.		CC This sequence represents the human BAK protein. The invention relates to a bcl homology domain (BH3 domain), derived from a proapoptotic member of the BCL-2 family. The BH3 polypeptide can be used in a method for promoting apoptosis in a target cell, especially where the cell is a cancer cell, a virus infected cell or an antibody producing cell. The BH3 polypeptide can be used in therapeutic compositions for treating disease including cancer, other lymphoproliferative conditions, arthritis, inflammation, and autoimmune diseases, which may result from the down regulation of cell death regulation.	
XX		CC Sequence 211 AA;	
PT New Bak-binding protein and related nucleic acid, vectors, transformed cells and antibodies - are useful for modulation of apoptosis in cancer, neuro-degeneration etc., also peptide fragments of Bak that interact with the protein.		CC Query Match 100.0%; Score 102; DB 2; Length 211;	
PT		CC Best Local Similarity 100.0%; Pred. No. 2.8e-09;	
CC		CC Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
CC		Db 70 TMGQVGRQLAIGDDINRY 89	
CC		RESULT 20	
CC		ID ABB8334	
CC		DB Human BAK protein sequence.	
CC		XX	
CC		AC ABB8334;	
CC		XX	
CC		DT 08-JAN-2003	(first entry)
CC		XX	
CC		Query Match 100.0%; Score 102; DB 2; Length 211;	
CC		Best Local Similarity 100.0%; Pred. No. 2.8e-09;	
CC		Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
CC		SQ Sequence 211 AA;	
CC		XX	
CC		Query Match 100.0%; Score 102; DB 2; Length 211;	
CC		Best Local Similarity 100.0%; Pred. No. 2.8e-09;	
CC		Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
CC		Db 70 TMGQVGRQLAIGDDINRY 89	

KW apoptosis; human.  
 OS Homo sapiens.  
 XX WO200274908-A2.  
 XX PD 26-SEP-2002.  
 XX PF 04-MAR-2002; 2002WO-US006757.  
 XX PR 02-MAR-2001; 2001US-027391P.  
 XX PA (MDSP-) MDS PROTEOMICS INC.  
 PI McFadden G, Moran MF;  
 XX Disclosure; Fig 11; 83pp; English.  
 DR 2002-740855/80.

XX PT Identifying agents which may be potentially pro-apoptotic or anti-apoptotic for treating acute and chronic neurodegenerative diseases, BAK and/or MLL proteins. The methods are useful for identifying agents which may be potentially pro-apoptotic or anti-apoptotic and for identifying MLL-interacting polypeptides, and in conducting a target or drug discovery system. The methods are useful for identifying agents capable of inhibiting MLL activity or which can mimic the activity of MLL by inhibiting the activity of BAK and which are therefore anti-apoptotic agents. Agents identified by the method as involved in regulation of apoptosis may be used in the development of therapeutic agents and methods, and drug screening assays, and in increasing the sensitivity of cancer cells to chemotherapeutic treatment of acute and chronic neurodegenerative diseases, e.g. stroke, Alzheimer's or Huntington's disease by drugs, and sensitization of cancer cells for drug /radiation-induced apoptosis by modulation of survival signals and viral transfer of apoptosis promoting genes. The present sequence represents a human BAK protein.  
 XX Sequence 211 AA;  
 CC -apoptotic or anti-apoptotic which involves determining the effect of a test agent on the complexes of BAK and/or MLL proteins. The methods are useful for identifying agents which may be potentially pro-apoptotic or anti-apoptotic and for identifying MLL-interacting polypeptides, and in conducting a target or drug discovery system. The methods are useful for identifying agents capable of inhibiting MLL activity or which can mimic the activity of MLL by inhibiting the activity of BAK and which are therefore anti-apoptotic agents. Agents identified by the method as involved in regulation of apoptosis may be used in the development of therapeutic agents and methods, and drug screening assays, and in increasing the sensitivity of cancer cells to chemotherapeutic treatment of acute and chronic neurodegenerative diseases, e.g. stroke, Alzheimer's or Huntington's disease by drugs, and sensitization of cancer cells for drug /radiation-induced apoptosis by modulation of survival signals and viral transfer of apoptosis promoting genes. The present sequence represents a human BAK protein.  
 XX Sequence 211 AA;

Query Match 100.0%; Score 102; DB 5; Length 211;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; OS Homo sapiens.  
 XX WO200300989-A2.  
 PD 16-JAN-2003.

XX RESULT 21  
 AAE37655  
 ID AAE37655 standard; protein; 211 AA.  
 XX AC AAE37655;  
 XX DT 27-AUG-2003 (first entry)  
 XX DE Bcl2 related protein #6.  
 XX KW Bcl2 related protein; growth; protein expression.  
 XX OS Unidentified.  
 XX PN WO2003040374-A1.  
 XX PD 15-MAY-2003.

PP 02-NOV-2001; 2001WO-US045553.  
 XX PR 02-NOV-2001; 2001WO-US045553.  
 XX PA (CENZ ) CENTOCOR INC.  
 XX PI Lee C, Ly C, Moore G, Shi X;  
 XX DR WPI; 2003-441576/41.  
 XX PT New protein expression enhancing Bcl2 related nucleic acid for producing commercially useful amounts of expressed protein, comprises a nucleic acid that encodes an expressible protein or at least one Bcl2 related protein.  
 XX PT Disclosure; Page 52-53; 64pp; English.  
 XX CC The invention relates to methods and compositions for enhanced protein expression and/or growth of cultured cells using co-transcription of at least one Bcl2 related protein encoding nucleic acid molecules. The invention is useful in providing enhanced growth of and/or protein production from cultured mammalian host cells used for the production of commercially useful amounts of expressed protein. The present sequence is Bcl2 related protein.  
 XX PS Sequence 211 AA;  
 Query Match 100.0%; Score 102; DB 6; Length 211;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; OS Homo sapiens.  
 XX QY 1 TMGQVGRQLAIGDDINRY 20  
 DB 70 TMGQVGRQLAIGDDINRY 89  
 XX RESULT 22  
 ABR47397  
 ID ABR47397 standard; protein; 211 AA.  
 XX AC ABR47397;  
 XX DT 12-JUN-2003 (first entry)  
 XX DB Breast cancer associated protein sequence SEQ ID NO:25.  
 XX KW Human; breast cancer; cytosstatic; gene therapy.  
 XX OS Homo sapiens.  
 XX PN WO200300989-A2.  
 XX PD 16-JAN-2003.  
 XX PR 21-JUN-2002; 2002WO-US019669.  
 XX PR 21-JUN-2001; 2001US-0293887P.  
 PR 27-JUL-2001; 2001US-030572P.  
 PR 18-JUL-2001; 2001US-030501P.  
 PR 25-SEP-2001; 2001US-032502P.  
 PR 05-MAR-2002; 2002US-036585P.  
 PR 14-MAY-2002; 2002US-0380391P.  
 XX PA (MILLI-) MILLENIUM PHARM INC.  
 XX PI Lillie J, Gannavarapu M, Glatt K, Hoersh S, Kamatkar S;  
 XX PI Merlans M, Monahan JE, Myer V, Wang Y, Xu Y, Zhao X, Meyers RE;  
 XX PI Bast RC, Hortobagyi GN, Pusztai L, Meric F, Sahn A, Mills GB;  
 XX DR WPI; 2003-210381/20.  
 XX DR N-PSDB; ACC50088.  
 XX PT Breast cancer diagnosis or treatment by comparing the level of expression

of a marker in a patient sample with that in the control non-breast cancer sample.

PT PT

XX SEQ ID NO 25; 128pp; English.

XX The present invention describes a method for assessing whether a patient is afflicted with breast cancer. The method comprises comparing the level of expression of a marker (gene/polypeptide) see ACC50076 to ACC50334 and ABR4786 to ABR47632 in a patient sample and the normal level of expression of the marker in a control non-breast cancer sample, where a significant increase in the level of expression of the marker in the patient sample and the normal level is an indication that the patient is afflicted with breast cancer. The breast cancer associated sequences from the present invention have cytostatic activities and can be used in gene therapy. The method is useful for diagnosing and treating breast cancer. N.B. The sequence data for this patient did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp://wipo.int/patent/publications/pct\\_sequences](http://wipo.int/patent/publications/pct_sequences)

XX Sequence 211 AA;

Query Match 100.0%; Score 102; DB 6; Length 211;  
Best Local Similarity 100.0%; Pred. No. 2.8e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TMGQVRQLAIGDDINRY 20  
Db 70 TMGQVRQLAIGDDINRY 89

RESULT 24

Query Match 100.0%; Score 102; DB 7; Length 211;  
Best Local Similarity 100.0%; Pred. No. 2.8e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TMGQVRQLAIGDDINRY 20  
Db 70 TMGQVRQLAIGDDINRY 89

RESULT 23

ADD93300 ID ADD93300 standard; protein; 211 AA.  
XX AC  
XX ADD93300;  
XX DT 29-JAN-2004 (first entry)  
XX DB Human pro-apoptotic protein Bak.  
XX KW Human; Bak; cytostatic; apoptosis.  
XX OS Homo sapiens.  
XX PN WO2003062828-A2.  
XX PD 31-JUL-2003.  
XX PP 17-JAN-2003; 2003WO-GB0000185.  
XX PR 17-JAN-2002; 2002GB-00000370.  
XX PA (UYMA-) UNIV VICTORIA MANCHESTER.  
XX PI Griffiths GJ;  
XX DR WPI: 2003-902664/82.  
XX Disclosure; SEQ ID NO 1; 16pp; English.

XX Griffiths GJ;

XX WPI: 2003-748015/70.

XX Determining potential effect of chemotherapeutic agents, useful for treating cancer, from their ability to induce conformational change in Bak protein.  
XX Disclosure; SEQ ID NO 1; 16pp; English.  
XX

The present sequence is the protein sequence of the human pro-apoptotic protein, Bak. A conformational change in the Bak protein is used in the method of the invention for determining the potential effectiveness of a chemotherapeutic compound for treating cancerous cells in a human or animal patient. The method involves: (i) exposing a sample of the cancerous cells taken from the patient to a chemotherapeutic compound, or combination of compounds; and (ii) assaying for a conformational change in the Bak protein of the cells. The conformational change is preferably determined at the N-terminus of Bak or in its BH1 domain, particularly

using a specific binding partner, such as an antibody, for the conformationally altered protein. Conformational change in Bak is a very early (and general) indicator of commitment to apoptosis, occurring before caspase activation, nuclear condensation or cellular blebbing, and is caused by agents that induce apoptosis by different mechanisms. Detecting commitment to apoptosis is a more accurate indicator of activity than cell death and the present method is quicker and simpler than known clonogenic assays.

SQ Sequence 211 AA;

Query Match 100.0%; Score 102; DB 7; Length 211;  
Best Local Similarity 100.0%; Pred. No. 2.8e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TMGQVRQLAIGDDINRY 20  
Db 70 TMGQVRQLAIGDDINRY 89

RESULT 24

Query Match 100.0%; Score 102; DB 7; Length 211;  
Best Local Similarity 100.0%; Pred. No. 2.8e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TMGQVRQLAIGDDINRY 20  
Db 70 TMGQVRQLAIGDDINRY 89

RESULT 24

Query Match 100.0%; Score 102; DB 7; Length 211;  
Best Local Similarity 100.0%; Pred. No. 2.8e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TMGQVRQLAIGDDINRY 20  
Db 70 TMGQVRQLAIGDDINRY 89

The invention relates to a method for detecting a chemotherapeutic activity in a compound other than an ecoposide, or in a combination of compounds. In the method of the invention, a cell that over expresses an anti-apoptotic protein is treated with at least one compound, and any change in the conformation of cellular Bak, indicative of chemotherapeutic activity, is detected. The anti-apoptotic protein is Bcl-2 or Bcl-XL, and is over expressed by transfecting the cells with a pCDNA3.1 vector that contains the anti-apoptotic-expressing sequence under control of the cytomegalovirus promoter. The method of the invention is used to identify, or screen for, chemotherapeutic agents for the treatment of cancer. The current sequence represents the human Bak amino acid sequence.

SQ Sequence 211 AA;

Query Match 100.0%; Score 102; DB 7; Length 211;

Best Local Similarity 100.0%; Pred. No. 2.8e-09;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TMGQVGRQLAIGDDINRY 20  
 Db 70 TMGQVGRQLAIGDDINRY 89

RESULT 25  
 ADL69726 standard; protein; 211 AA.  
 ID ADL69726  
 XX AC ADL69726;  
 XX DT 20-MAY-2004 (first entry)  
 XX DE Human Bcl2 related protein #6.  
 XX KW Bcl2 related protein; therapeutic protein; human.  
 XX OS Homo sapiens.  
 XX PN US2004043028-A1.  
 XX PD 04-MAR-2004.  
 XX PF 02-NOV-2001; 2001US-00003632.  
 XX PR 02-NOV-2001; 2001US-00003632.  
 XX PA (LBECL/) LEE C.  
 XX PA (SHIX/) SHI X.  
 XX PA (LYCC/) LY C.  
 XX PA (MOOR/) MOORE G.  
 XX PT Lee C, Shi X, LY C, Moore G;  
 XX DR 2004-225672/21.  
 XX PT New Bcl2 encoding nucleic acids for enhancing growth and/or production of therapeutic or diagnostic proteins from cultured mammalian host cells.  
 XX PS Disclosure; SEQ ID NO 6; 42pp; English.  
 XX CC The invention relates to a protein expression enhancing Bcl2 related nucleic acid comprising a first nucleic acid encoding at least one expressible protein and a second nucleic acid encoding at least one Bcl2 related protein, where expression of the expressible protein is enhanced by transcription or translation of the second nucleic acid. The composition and methods are useful for enhancing growth and/or production of therapeutic or diagnostic proteins from cultured mammalian host cells. The present sequence is human Bcl2 related protein.  
 XX SQ Sequence 211 AA;

Query Match 100.0%; Score 102; DB 8; Length 211;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Gaps 0;

Qy 1 TMGQVGRQLAIGDDINRY 20  
 Db 70 TMGQVGRQLAIGDDINRY 89

RESULT 26  
 ADP04114 standard; protein; 211 AA.  
 ID ADP04114;  
 XX AC ADP04114;  
 XX DT 09-SEP-2004 (first entry)  
 XX DE Human colon specific protein SEQ ID NO:95.  
 XX KW human; colon specific nucleic acid; CSNA; colon specific protein; CSP; cytosatic; vaccine; gene therapy; colon cancer.

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OM protein - protein search, using sw model

Run on: January 25, 2005, 10:10:46 ; Search time 97.5 Seconds  
(without alignments)

74.111 Million cell updates/sec

Title: US-09-828-870-36

Perfect score: 102

Sequence: 1 TMGQVGRQLAIIGDDINRY 20

Scoring table: BL0SUM62

Gapext 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

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RESULT 1 US-09-828-870-36

Sequence 36, Application US/09-828-870-36

Publication No. US20040054129A1

GENERAL INFORMATION:

APPLICANT: CHITTENDEN, Thomas D. ; and

LUTZ, Robert J.

TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hale and Dorr

STREET: 1455 Pennsylvania Avenue, N.W.

CITY: Washington

STATE: D.C.

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09-828-870-36

FILING DATE: 10-Apr-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/236,385

FILING DATE: 25-JANUARY-1999

ATTORNEY/AGENT INFORMATION:

NAME: WIXON, HENRY N.

REGISTRATION NUMBER: 32,073

(C) ATTORNEY DOCKET NO. 104322-147CIP

TELECOMMUNICATION INFORMATION:

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TELEFAX: 202-942-8484

INFORMATION FOR SEQ ID NO: 36

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	102	100.0	20	11 US-09-828-870-36	Sequence 36, Appl
2	102	100.0	28	11 US-09-828-870-2	Sequence 2, Appl
3	102	100.0	28	11 US-09-828-870-18	Sequence 18, Appl
4	102	100.0	36	11 US-09-828-870-14	Sequence 14, Appl
5	102	100.0	210	14 US-10-101-482-22	Sequence 20, Appl
6	102	100.0	211	14 US-10-101-482-7	Sequence 7, Appl
7	102	100.0	211	14 US-10-101-482-9	Sequence 9, Appl
8	102	100.0	211	14 US-10-101-482-10	Sequence 10, Appl
9	102	100.0	211	14 US-10-101-482-11	Sequence 11, Appl
10	102	100.0	211	14 US-10-101-482-12	Sequence 2, Appl
11	102	100.0	211	14 US-10-101-482-13	Sequence 25, Appl
12	102	100.0	211	15 US-10-003-632C-6	Sequence 6, Appl
13	102	100.0	211	17 US-10-025-282-34	Sequence 34, Appl

SEQUENCE CHARACTERISTICS:  
 LENGTH: 20 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear

MOLECULE TYPE: peptide  
 SEQUENCE DESCRIPTION: SEQ ID NO: 36  
 US-09-828-870-36

Query Match 100.0%; Score 102; DB 11; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TMGQYGRQIAIGGDDINRY 20  
 Db 1 TMGQYGRQIAIGGDDINRY 20

RESULT 2  
 US-09-828-870-2  
 Publication No. US-09-828-870-2  
 Sequence 2, Application US/09828870

GENERAL INFORMATION:  
 APPLICANT: CHITTENDEN, Thomas D.; and  
 LUTZ, Robert J.

TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH  
 MODULATE APOPTOSIS

NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:  
 STREET: Hale and Dorr  
 CITY: 1455 Pennsylvania Avenue, N.W.  
 STATE: D.C.  
 ZIP: 20004

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09-828-870  
 FILING DATE: 10-Apr-2001  
 CLASSIFICATION: <Unknown>  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 09/236,385  
 FILING DATE: 25-JANUARY-1999  
 ATTORNEY/AGENT INFORMATION:  
 NAME: WIXON, HENRY N.  
 REGISTRATION NUMBER: 32,073  
 (C) ATTORNEY DOCKET NO. 104322.147CIP

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-942-8400  
 TELEFAX: 202-942-8484

INFORMATION FOR SEQ ID NO: 18:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 28 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
 US-09-828-870-18

Query Match 100.0%; Score 102; DB 11; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TMGQYGRQIAIGGDDINRY 20  
 Db 4 TMGQYGRQIAIGGDDINRY 23

RESULT 4  
 US-09-828-870-14  
 Sequence 14, Application US/09828870  
 Publication No. US-09-828-870-14

GENERAL INFORMATION:  
 APPLICANT: CHITTENDEN, Thomas D.; and  
 LUTZ, Robert J.

TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH  
 MODULATE APOPTOSIS

NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:  
 STREET: Hale and Dorr  
 CITY: 1455 Pennsylvania Avenue, N.W.  
 STATE: D.C.  
 ZIP: 20004

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09-828-870-18

Query Match 100.0%; Score 102; DB 11; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TMGQYGRQIAIGGDDINRY 20  
 Db 4 TMGQYGRQIAIGGDDINRY 23

RESULT 3  
 US-09-828-870-18  
 Sequence 18, Application US/09828870

FILING DATE: 10-Apr-2001  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/236,385  
 FILING DATE: 25-JANUARY-1999  
 ATTORNEY/AGENT INFORMATION:  
 NAME: WILSON, HENRY N.  
 REGISTRATION NUMBER: 32,073  
 (C) ATTORNEY DOCKET NO. 104322.147CIP  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-942-8400  
 TELEFAX: 202-942-8484  
 INFORMATION FOR SEQ ID NO: 14:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 36 base pairs  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide  
 SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
 US-09-828-870-14

Query Match 100.0%; Score 102; DB 14;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-08;  
 Matches 20; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Qy 1 TMGGGRQLAIIGDDINRY 20  
 Db 70 TMGGGRQLAIIGDDINRY 89

RESULT 5  
 US-10-101-482-22  
 ; Sequence 22, Application US/10101482  
 ; Publication No. US20030008837A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KIEFER, MICHAEL C.  
 ; BARR, PHILIP J.  
 ; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA  
 ; ENCODING THE PROTEINS AND METHODS OF USE THEREOF  
 ; NUMBER OF SEQUENCES: 22  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: MORRISON & FOERSTER  
 ; STREET: 755 Page Mill Road  
 ; CITY: Palo Alto  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94304-1018  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/101,482  
 FILING DATE: 18-Mar-2002  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/320,157  
 FILING DATE: 07-OCT-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: LEINHARDT, SUSAN K.  
 REGISTRATION NUMBER: 33,943  
 REFERENCE/DOCKET NUMBER: 23647-20007.20  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 813-5600  
 TELEFAX: (415) 494-0792

INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 211 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
 US-10-101-482-7

Query Match 100.0%; Score 102; DB 14;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-08;  
 Matches 20; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Qy 1 TMGGGRQLAIIGDDINRY 20  
 Db 70 TMGGGRQLAIIGDDINRY 89

RESULT 7  
 US-10-101-482-9  
 ; Sequence 9, Application US/10101482  
 ; Publication No. US20030008837A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KIEFER, MICHAEL C.

TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA ENCODING THE PROTEINS AND METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/101,482

FILING DATE: 18-Mar-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/320,157

FILING DATE: 07-OCT-1994

ATTORNEY/AGENT INFORMATION:

NAME: LEHNHARDT, SUSAN K.

REGISTRATION NUMBER: 33,943

REFERENCE/DOCKET NUMBER: 23647-20007.20

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 813-5600

TELEFAX: (415) 494-0792

TELEX: 706141

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 211 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-10-101-482-9

RESULT 8

Query Match 100.0%; Score 102; DB 14; Length 211;

Best Local Similarity 100.0%; Pred. No. 1.5e-08;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TMGGVGRQLAIGDDINRY 20

Db 70 TMGGVGRQLAIGDDINRY 89

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/101,482

FILING DATE: 18-Mar-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/320,157

FILING DATE: 07-OCT-1994

ATTORNEY/AGENT INFORMATION:

NAME: LEHNHARDT, SUSAN K.

REGISTRATION NUMBER: 33,943

REFERENCE/DOCKET NUMBER: 23647-20007.20

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 813-5600

TELEFAX: (415) 494-0792

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 211 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear  
 SEQ ID DESCRIPTION: SEQ ID NO: 11:  
 US-10-101-482-11

Query Match 100.0%; Score 102; DB 14; Length 211;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TMGQYGRQLAIGDDINRY 20  
 Db 70 TMGQYGRQLAIGDDINRY 89

RESULT 10  
 US-10-189-294-2  
 Sequence 2, Application US/10189-294  
 Publication No. US20030060515A1  
 GENERAL INFORMATION:  
 APPLICANT: Kietter, Michael C.  
 GIBSON, Helen L.  
 FITPATRICK, Paul A.  
 BARR, Phillip J.

TITLE OF INVENTION: A NOVEL BAK BINDING PROTEIN, DNA  
 ENCODING THE PROTEIN, AND METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: BROWN, THERESA A.  
 STREET: 1560 Broadway, Suite 1200  
 CITY: Denver  
 STATE: CO  
 COUNTRY: USA  
 ZIP: 80202

COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/189,294  
 FILING DATE: 01-Jul-2002  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/09/381,488  
 FILING DATE: 11-Feb-2000

ATTORNEY/AGENT INFORMATION:  
 NAME: BROWN, THERESA A.  
 REGISTRATION NUMBER: 32,547  
 REFERENCE DOCKET NUMBER: 4:147-15-PUS

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (303) 863-9700  
 TELEFAX: (303) 863-0223

INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 211 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 US-10-189-294-2

Query Match 100.0%; Score 102; DB 14; Length 211;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TMGQYGRQLAIGDDINRY 20  
 Db 70 TMGQYGRQLAIGDDINRY 89

RESULT 11  
 US-10-177-293-25  
 Sequence 25, Application US/10177293  
 Publication No. US20030124128A1

Query Match 100.0%; Score 102; DB 15; Length 211;

Query Match 100.0%; Score 102; DB 14; Length 211;

Query Match 100.0%; Score 102; DB 14; Length 211;

Query Match 100.0%; Score 102; DB 15; Length 211;

Best Local Similarity 100.0%; Pred. No. 1.5e-08; Mismatches 0; Indels 0; Gaps 0;

ATTORNEY/AGENT INFORMATION:  
NAME: WIXON, HENRY N.  
REGISTRATION NUMBER: 32,073  
(C) ATTORNEY DOCKET NO. 104322.147CIP

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-942-8400  
TELEFAX: 202-942-8484

INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
TOPOLOGY: Linear  
MOLECULE TYPE: Peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 35:  
US-09-828-870-35

Query Match 95.1%; Score 97; DB 11; Length 19;  
Best Local Similarity 100.0%; Pred. No. 6.7e-09;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 MGQVGRQLAIGDDINRY 20  
Db 1 MGQVGRQLAIGDDINRY 19

RESULT 15  
US-10-805-282-34  
Sequence 34, Application US/10825282  
Publication No. US20040224389A1  
GENERAL INFORMATION:  
PRIORITY INFORMATION:  
APPLICANT: 3921-1-1-1  
TITLE OF INVENTION: VIRAL VECTORS ENCODING APOPTOSIS-INDUCING PROTEINS AND METHODS FOR MAKING AND USING THE SAME  
FILE REFERENCE: 3921-1-1-1  
CURRENT APPLICATION NUMBER: US/10/825,282  
PRIORITY APPLICATION NUMBER: US/09/456,357  
PRIOR FILING DATE: 1995-12-08  
PRIOR APPLICATION NUMBER: 60/134,416  
PRIOR FILING DATE: 1999-05-17  
PRIOR APPLICATION NUMBER: 09/087,195  
PRIOR FILING DATE: 1998-05-29  
PRIOR APPLICATION NUMBER: 08/378,507  
PRIOR FILING DATE: 1995-01-26  
PRIOR APPLICATION NUMBER: 08/250,478  
PRIOR FILING DATE: 1994-05-27  
NUMBER OF SEQ ID NOS: 50  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO: 34  
LENGTH: 211  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-825-282-34

Query Match 100.0%; Score 102; DB 17; Length 211;  
Best Local Similarity 100.0%; Pred. No. 1.5e-08; Mismatches 0; Indels 0; Gaps 0;

ATTORNEY/AGENT INFORMATION:  
NAME: BROWN, THERESE A.  
REGISTRATION NUMBER: US0030060615A1  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

INFORMATION FOR SEQ ID NO: 10189294:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
TOPOLOGY: Linear  
FEATURE: Protein  
NAME/KEY: Protein  
LOCATION: 1..117

CURRENT APPLICATION DATA:  
APPLICANT: Kiefer, Michael C.  
PRIORITY APPLICATION NUMBER: US/09/381,488  
FILING DATE: 11-Feb-2000  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWN, THERESE A.  
REGISTRATION NUMBER: 32,547  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

INFORMATION FOR SEQ ID NO: 10189294:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 117 amino acids  
TYPE: amino acid  
TOPOLOGY: Linear  
FEATURE: Protein  
NAME/KEY: Protein  
LOCATION: 1..117

NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWN, THERESE A.  
STREET: 1560 Broadway, Suite 1200  
CITY: Denver  
STATE: CO  
COUNTRY: USA  
ZIP: 80202

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICANT: Fitzpatrick, Paul A.  
PRIORITY APPLICATION NUMBER: US/10/189,294  
FILING DATE: 01-Jul-2002  
CLASIFICATION: <Unknown>  
PRIORITY APPLICATION NUMBER: US/09/381,488  
FILING DATE: 11-Feb-2000

ATTORNEY/AGENT INFORMATION:  
NAME: BROWN, THERESE A.  
REGISTRATION NUMBER: 32,547  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

INFORMATION FOR SEQ ID NO: /note- "Bak (delta) 2 (delta) TM":  
SEQUENCE CHARACTERISTICS:  
LENGTH: 117 amino acids  
TYPE: amino acid  
TOPOLOGY: Linear  
FEATURE: Protein  
NAME/KEY: Protein  
LOCATION: 1..117

NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr  
STREET: 1455 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
ZIP: 20004

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICANT: LUTZ, Robert J.; and  
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH MODULATE APOPTOSIS  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr  
STREET: 1455 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
ZIP: 20004

INFORMATION FOR SEQ ID NO: /note- "Bak (delta) 2 (delta) TM":  
SEQUENCE CHARACTERISTICS:  
LENGTH: 117 amino acids  
TYPE: amino acid  
TOPOLOGY: Linear  
FEATURE: Protein  
NAME/KEY: Protein  
LOCATION: 1..117

NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LUTZ, Robert J.; and  
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH MODULATE APOPTOSIS  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr  
STREET: 1455 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
ZIP: 20004

INFORMATION FOR SEQ ID NO: /note- "Bak (delta) 2 (delta) TM":  
SEQUENCE CHARACTERISTICS:  
LENGTH: 117 amino acids  
TYPE: amino acid  
TOPOLOGY: Linear  
FEATURE: Protein  
NAME/KEY: Protein  
LOCATION: 1..117

;US-10-189-294-4  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-189-294-4 ; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Query Match	95.1%	Score	97;	DB	14;	Length	117;
Best Local Similarity	100.0%	Pred. No.	5e-08;				
Matches	19;	Conservative	0;	Mismatches	0;	Indels	

Qy	2	MGQVGRQLAIIGDDINRRY	20
	1	MGQVGRQLAIIGDDINRRY	19
Db			

Search completed: January 25, 2005, 10:31:00  
Job time : 98.5 SECS

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OM protein - protein search, using sw model

Run on: January 26, 2005, 00:02:31 ; Search time 38 Seconds

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0 %

Maximum Match 100 %

Listing First 45 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/picodata/1/iaa/5A\_COMB.pep:\*

2: /cgn2\_6/picodata/1/iaa/5B\_COMB.pep:\*

3: /cgn2\_6/picodata/1/iaa/6A\_COMB.pep:\*

4: /cgn2\_6/picodata/1/iaa/6B\_COMB.pep:\*

5: /cgn2\_6/picodata/1/iaa/PCUTS\_COMB.pep:\*

6: /cgn2\_6/picodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	102	100.0	20	3	US-09-336-385A-36	Sequence 36, Appli	
2	102	100.0	27	4	US-09-544-664B-4	Sequence 4, Appli	
3	102	100.0	28	1	US-08-440-391-2	Sequence 2, Appli	
4	102	100.0	28	1	US-08-440-391-18	Sequence 18, Appli	
5	102	100.0	28	2	US-08-908-597A-2	Sequence 2, Appli	
6	102	100.0	28	2	US-08-908-597A-18	Sequence 18, Appli	
7	102	100.0	28	3	US-09-336-385A-2	Sequence 2, Appli	
8	102	100.0	28	3	US-09-336-385A-18	Sequence 18, Appli	
9	102	100.0	28	5	PCT-US96-06122-2	Sequence 2, Appli	
10	102	100.0	28	5	PCT-US96-06122-18	Sequence 18, Appli	
11	102	100.0	36	1	US-08-440-391-14	Sequence 14, Appli	
12	102	100.0	36	2	US-08-908-597A-14	Sequence 14, Appli	
13	102	100.0	36	3	US-09-336-385A-14	Sequence 14, Appli	
14	102	100.0	36	5	PCT-US96-06122-14	Sequence 14, Appli	
15	102	100.0	152	1	US-08-471-058-22	Sequence 22, Appli	
16	102	100.0	210	3	US-08-471-057-22	Sequence 22, Appli	
17	102	100.0	210	4	US-08-470-865-22	Sequence 22, Appli	
18	102	100.0	211	1	US-08-321-071A-16	Sequence 16, Appli	
19	102	100.0	211	1	US-08-471-058-7	Sequence 7, Appli	
20	102	100.0	211	1	US-08-471-058-9	Sequence 9, Appli	
21	102	100.0	211	1	US-08-471-058-10	Sequence 10, Appli	
22	102	100.0	211	1	US-08-471-058-11	Sequence 11, Appli	
23	102	100.0	211	2	US-08-944-510-2	Sequence 2, Appli	
24	102	100.0	211	3	US-08-944-510-4	Sequence 4, Appli	
25	102	100.0	211	3	US-08-471-057-7	Sequence 7, Appli	
26	102	100.0	211	3	US-08-471-057-9	Sequence 9, Appli	
27	100.0		211	3	US-08-471-057-10	Sequence 10, Appli	

## ALIGNMENTS

RESULT 1  
US-09-336-385A-36  
; Sequence 36, Application US/09236385A  
; Patent No. 622165

GENERAL INFORMATION:  
APPLICANT: CHITTENDEN, Thomas D. ; and  
LUTZ, Robert J.  
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH  
MODULATE APOPTOSIS  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr  
STREET: 1455 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/236,385A  
FILING DATE: 25-Jan-1999  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: WIXON, HENRY N.  
REGISTRATION NUMBER: 32,073  
(C) ATTORNEY DOCKET NO. 104322.147CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-942-8400  
TELEFAX: 202-942-8484  
INFORMATION FOR SEQ ID NO: 36  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 36  
US-09-236-385A-36

Query Match Score 102; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.9e-11;  
Matches 20; Conserv. 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TMGQYGRQIAIGDDINRRY 20  
Db 1 TMGQYGRQIAIGDDINRRY 20

RESULT 2  
 US-09-544-664B-4  
 Sequence 4, Application US/09544664B  
 / Patent No. 6733280  
 / GENERAL INFORMATION:  
 / APPLICANT: Huang, Zhiwei  
 / APPLICANT: Wang, Jialun  
 / APPLICANT: Zhang, Zhijia  
 / APPLICANT: Shan, Simei  
 / APPLICANT: Lu, Zhiyan  
 / FILE REFERENCE: Enhancement of Peptide Cellular Uptake  
 / CURRENT APPLICATION NUMBER: US/09/544, 664B  
 / CURRENT FILING DATE: 2000-04-06  
 / PRIOR APPLICATION NUMBER: PCT/US00/0352  
 / PRIOR FILING DATE: 2000-04-06  
 / PRIOR APPLICATION NUMBER: 60/128, 202  
 / PRIOR FILING DATE: 1999-04-07  
 / NUMBER OF SEQ ID NOS: 58  
 / SOFTWARE: PatentIn Ver. 2.1  
 / SEQ ID NO 4  
 / LENGTH: 27  
 / TYPE: PRT  
 / FEATURE: Artificial Sequence  
 / OTHER INFORMATION: Description of Artificial Sequence: Peptide  
 / OTHER INFORMATION: segment from BH3 domain of a Bcl-2 superfamily  
 / OTHER INFORMATION: polypeptide  
 / SEQ ID NO 4  
 / LENGTH: 27

Query Match 100.0%; Score 102; DB 4; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-10;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 TMGQVGRQLAIGDDINRY 20  
 Db 4 TMGQVGRQLAIGDDINRY 23

RESULT 3  
 US-08-440-391-2  
 / Sequence 2, Application US/08440391  
 / Patent No. 5656725  
 / GENERAL INFORMATION:  
 / APPLICANT: CHITTENDEN, Thomas D.; and  
 / APPLICANT: LUTZ, Robert J.  
 / FILE REFERENCE: 202-942-8484  
 / TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH  
 / NUMBER OF SEQUENCES: 34  
 / SEQUENCE CHARACTERISTICS:  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSEE: Hale and Dorr  
 / CITY: Washington Avenue, N.W.  
 / STATE: D.C.  
 / ZIP: 20004  
 / COMPUTER READABLE FORM:  
 / MEDIUM TYPE: Floppy disk  
 / COMPUTER: IBM PC compatible  
 / OPERATING SYSTEM: PC-DOS/MS-DOS  
 / SOFTWARE: PatentIn Release #1.0, Version #1.25  
 / CURRENT APPLICATION DATA:  
 / APPLICATION NUMBER: US/08/440, 391  
 / FILING DATE: 12-MAY-1995  
 / CLASSIFICATION: 435  
 / ATTORNEY/AGENT INFORMATION:  
 / NAME: WIXON, HENRY N.  
 / REGISTRATION NUMBER: 32, 073  
 / REFERENCE/DOCKET NUMBER: 104322.147  
 / TELECOMMUNICATION INFORMATION:  
 / TELEPHONE: 202-942-8400  
 / TELEFAX: 202-942-8484  
 / INFORMATION FOR SEQ ID NO: 18:  
 / LENGTH: 28 amino acids  
 / TYPE: amino acid  
 / TOPOLGY: linear  
 / MOLECULE TYPE: peptide  
 / SEQ ID NO 4  
 / LENGTH: 27

RESULT 4  
 US-08-440-391-18

Query Match 100.0%; Score 102; DB 1; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-10;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 TMGQVGRQLAIGDDINRY 20  
 Db 4 TMGQVGRQLAIGDDINRY 23

RESULT 4  
 US-08-440-391-18  
 / Sequence 18, Application US/08440391  
 / Patent No. 5656725  
 / GENERAL INFORMATION:  
 / APPLICANT: CHITTENDEN, Thomas D.; and  
 / APPLICANT: LUTZ, Robert J.  
 / FILE REFERENCE: 202-942-8484  
 / TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH  
 / NUMBER OF SEQUENCES: 34  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSEE: Hale and Dorr  
 / CITY: 1455 Pennsylvania Avenue, N.W.  
 / STATE: D.C.  
 / ZIP: 20004  
 / COMPUTER READABLE FORM:  
 / MEDIUM TYPE: Floppy disk  
 / COMPUTER: IBM PC compatible  
 / OPERATING SYSTEM: PC-DOS/MS-DOS  
 / SOFTWARE: PatentIn Release #1.0, Version #1.25  
 / CURRENT APPLICATION DATA:  
 / APPLICATION NUMBER: US/08/440, 391  
 / FILING DATE: 12-MAY-1995  
 / CLASSIFICATION: 435  
 / ATTORNEY/AGENT INFORMATION:  
 / NAME: WIXON, HENRY N.  
 / REGISTRATION NUMBER: 32, 073  
 / REFERENCE/DOCKET NUMBER: 104322.147  
 / TELECOMMUNICATION INFORMATION:  
 / TELEPHONE: 202-942-8400  
 / TELEFAX: 202-942-8484  
 / INFORMATION FOR SEQ ID NO: 18:  
 / LENGTH: 28 amino acids  
 / TYPE: amino acid  
 / TOPOLGY: linear  
 / MOLECULE TYPE: peptide  
 / SEQ ID NO 4  
 / LENGTH: 27

RESULT 5  
 US-08-908-597A-2  
 / Sequence 2, Application US/08908597A  
 / Patent No. 5863705  
 / GENERAL INFORMATION:  
 / APPLICANT: CHITTENDEN, Thomas D.; and  
 / APPLICANT: LUTZ, Robert J.  
 / FILE REFERENCE: 202-942-8484  
 / TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH  
 / NUMBER OF SEQUENCES: 34  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSEE: Hale and Dorr  
 / CITY: Washington Avenue, N.W.  
 / STATE: D.C.  
 / ZIP: 20004  
 / COMPUTER READABLE FORM:  
 / MEDIUM TYPE: Floppy disk  
 / COMPUTER: IBM PC compatible  
 / OPERATING SYSTEM: PC-DOS/MS-DOS  
 / SOFTWARE: PatentIn Release #1.0, Version #1.25  
 / CURRENT APPLICATION DATA:  
 / APPLICATION NUMBER: US/08/440, 391  
 / FILING DATE: 12-MAY-1995  
 / CLASSIFICATION: 435  
 / ATTORNEY/AGENT INFORMATION:  
 / NAME: WIXON, HENRY N.  
 / REGISTRATION NUMBER: 32, 073  
 / REFERENCE/DOCKET NUMBER: 104322.147  
 / TELECOMMUNICATION INFORMATION:  
 / TELEPHONE: 202-942-8400  
 / TELEFAX: 202-942-8484  
 / INFORMATION FOR SEQ ID NO: 2:  
 / SEQUENCE CHARACTERISTICS:

NUMBER OF SEQUENCES: 34  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Hale and Dorr  
 STREET: 1455 Pennsylvania Avenue, N.W.  
 CITY: Washington  
 STATE: D.C.  
 ZIP: 20004  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk.  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/908,597A.  
 FILING DATE:  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/440,391  
 FILING DATE: 12-MAY-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: WIXON, HENRY N.  
 REGISTRATION NUMBER: 32,073  
 REFERENCE DOCKET NUMBER: 104322.147  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-942-8400  
 TELEFAX: 202-942-8484  
 INFORMATION FOR SEQ ID NO:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 28 amino acid  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-908-597A-2

Query Match 100.0%; Score 102; DB 2; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-10;  
 Matches 20; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Query Match 100.0%; Score 102; DB 2; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-10;  
 Matches 20; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

RESULT 6  
 US-08-908-597A-18  
 Sequence 18, Application US/08/908,597A  
 Patent No. 5863795  
 GENERAL INFORMATION:  
 APPLICANT: CHITTENDEN, Thomas D.; and  
 ATTORNEY: LUTZ, Robert J.  
 TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH  
 NUMBER OF SEQUENCES: 34  
 TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH  
 NUMBER OF SEQUENCES: 34  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Hale and Dorr  
 STREET: 1455 Pennsylvania Avenue, N.W.  
 CITY: Washington  
 STATE: D.C.  
 ZIP: 20004  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/236,385A  
 FILING DATE: 25-Jan-1999  
 CLASSIFICATION: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: WIXON, HENRY N.  
 REGISTRATION NUMBER: 32,073  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-942-8400  
 TELEFAX: 202-942-8484  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 28 amino acid  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 US-09-236-385A-2

Query Match 100.0%; Score 102; DB 3; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-10;  
 Matches 20; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Query Match 100.0%; Score 102; DB 3; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-10;  
 Matches 20; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

RESULT 7  
 US-09-236-385A-2  
 Sequence 2, Application US/09/236,385A  
 Patent No. 6221615  
 GENERAL INFORMATION:  
 APPLICANT: CHITTENDEN, Thomas D.; and  
 ATTORNEY: LUTZ, Robert J.  
 TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH  
 NUMBER OF SEQUENCES: 41  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Hale and Dorr  
 STREET: 1455 Pennsylvania Avenue, N.W.  
 CITY: Washington  
 STATE: D.C.  
 ZIP: 20004  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/236,385A  
 FILING DATE: 25-Jan-1999  
 CLASSIFICATION: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: WIXON, HENRY N.  
 REGISTRATION NUMBER: 32,073  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-942-8400  
 TELEFAX: 202-942-8484  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 28 amino acid  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 US-09-236-385A-2

Query Match 100.0%; Score 102; DB 3; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-10;  
 Matches 20; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Query Match 100.0%; Score 102; DB 3; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-10;  
 Matches 20; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

RESULT 8  
 US-09-236-385A-2

US-09-236-385A-18  
 / Sequence 18, Application US/09236385A  
 / GENERAL INFORMATION:  
 / APPLICANT: CHITTENDEN, Thomas D.; and  
 / LUTZ, Robert J.  
 / TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH  
 / MODULATE APOPTOSIS  
 / NUMBER OF SEQUENCES: 41  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSEE: Hale and Dorr  
 / STREET: 1455 Pennsylvania Avenue, N.W.  
 / CITY: Washington  
 / STATE: D.C.  
 / ZIP: 20004  
 / COMPUTER READABLE FORM:  
 / MEDIUM TYPE: Floppy disk  
 / COMPUTER: IBM PC compatible  
 / OPERATING SYSTEM: PC-DOS/MS-DOS  
 / SOFTWARE: Patentin Release #1.0, Version #1.25  
 / CURRENT APPLICATION DATA:  
 / APPLICATION NUMBER: US/09/236,385A  
 / FILING DATE: 25-Jan-1999  
 / CLASSIFICATION: <Unknown>  
 / ATTORNEY/AGENT INFORMATION:  
 / NAME: WIXON, HENRY N.  
 / REGISTRATION NUMBER: 32,073  
 / (C) ATTORNEY DOCKET NO. 104322.147CIP  
 / TELECOMMUNICATION INFORMATION:  
 / TELEPHONE: 202-942-8400  
 / TELEFAX: 202-942-8484  
 / INFORMATION FOR SEQ ID NO: 18:  
 / SEQUENCE CHARACTERISTICS:  
 / LENGTH: 28 amino acids  
 / TYPE: amino acid  
 / TOPOLOGY: linear  
 / MOLECULE TYPE: Peptide  
 / SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
 / US-09-236-385A-18  
 / Query Match 100.0%; Score 102; DB 3; Length 28;  
 / Best Local Similarity 100.0%; Pred. No. 1.2e-10;  
 / Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 /  
 / Qy 1 TMGQVGRQLAIGDDINRY 20  
 / Db 4 TMGQVGRQLAIGDDINRY 23  
 /  
 / RESULT 9  
 / PCT-US96-06122-2  
 / Sequence 2, Application PC/TUS9606122  
 / GENERAL INFORMATION:  
 / APPLICANT: IMMUNOGEN, INC.  
 / TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH  
 / MODULATE APOPTOSIS  
 / NUMBER OF SEQUENCES: 34  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSEE: Hale and Dorr  
 / STREET: 1455 Pennsylvania Avenue, N.W.  
 / CITY: Washington  
 / STATE: D.C.  
 / ZIP: 20004  
 / COMPUTER READABLE FORM:  
 / MEDIUM TYPE: Floppy disk  
 / COMPUTER: IBM PC compatible  
 / OPERATING SYSTEM: PC-DOS/MS-DOS  
 / SOFTWARE: Patentin Release #1.0, Version #1.25  
 / CURRENT APPLICATION DATA:  
 / APPLICATION NUMBER: PCT/TUS96/06122  
 / FILING DATE: HEREWITH  
 / CLASSIFICATION:  
 / PRIOR APPLICATION DATA:  
 / APPLICATION NUMBER: US 08/440,391  
 / FILING DATE: 12-MAY-1995  
 / CLASSIFICATION:  
 / ATTORNEY/AGENT INFORMATION:  
 / NAME: WIXON, HENRY N.  
 / REGISTRATION NUMBER: 32,073  
 / REINVENTION NUMBER: 104322.147PCT  
 / TELECOMMUNICATION INFORMATION:  
 / TELEPHONE: 202-942-8400  
 / TELEFAX: 202-942-8484  
 / INFORMATION FOR SEQ ID NO: 18:  
 / SEQUENCE CHARACTERISTICS:  
 / LENGTH: 28 amino acids  
 / TYPE: amino acid  
 / TOPOLOGY: linear  
 / MOLECULE TYPE: Peptide  
 / PCT-US96-06122-18  
 / Query Match 100.0%; Score 102; DB 5; Length 28;  
 / Best Local Similarity 100.0%; Pred. No. 1.2e-10;  
 / Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 /  
 / PCT-US96-06122-2  
 / Sequence 2, Application PC/TUS9606122  
 / GENERAL INFORMATION:  
 / APPLICANT: IMMUNOGEN, INC.  
 / TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH  
 / MODULATE APOPTOSIS  
 / NUMBER OF SEQUENCES: 34  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSEE: Hale and Dorr  
 / STREET: 1455 Pennsylvania Avenue, N.W.  
 / CITY: Washington  
 / STATE: D.C.  
 / ZIP: 20004  
 / COMPUTER READABLE FORM:  
 / MEDIUM TYPE: Floppy disk  
 / COMPUTER: IBM PC compatible  
 / OPERATING SYSTEM: PC-DOS/MS-DOS  
 / SOFTWARE: Patentin Release #1.0, Version #1.25  
 / CURRENT APPLICATION DATA:  
 / APPLICATION NUMBER: PCT/TUS96/06122  
 / FILING DATE: HEREWITH  
 / CLASSIFICATION:  
 / PRIOR APPLICATION DATA:  
 /

OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/908,597A  
 FILING DATE:  
 CLASSIFICATION: 530  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US/08/440,391  
 FILING DATE: 12-MAY-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: WIXON, HENRY N.  
 REGISTRATION NUMBER: 32,073  
 REFERENCE/DOCKET NUMBER: 104322.147  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-942-8400  
 TELEFAX: 202-942-8484  
 INFORMATION FOR SEQ ID NO: 14:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 36  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-908-597A-14  
 Query Match Similarity 100.0%; Score 102; DB 2; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-10; Mismatches 0; Indels 0; Gaps 0;  
 Matches 20; Conservative 0;  
 Qy 1 TMGQVGRQLAIGDDINRY 20  
 Db 6 TMGQVGRQLAIGDDINRY 25  
 RESULT 13  
 US-09-236-385A-14  
 Query Match Similarity 100.0%; Score 102; DB 2; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-10; Mismatches 0; Indels 0; Gaps 0;  
 Matches 20; Conservative 0;  
 Qy 1 TMGQVGRQLAIGDDINRY 20  
 Db 6 TMGQVGRQLAIGDDINRY 25  
 RESULT 14  
 US/09/236/385A  
 Sequence 14, Application US/09/236/385A  
 Patent No. 6221615  
 GENERAL INFORMATION:  
 APPLICANT: CHITTENDEN, Thomas D.; and  
 LUTZ, Robert J.  
 TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH  
 MODULATE APOPTOSIS  
 NUMBER OF SEQUENCES: 34  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Hale and Dorr  
 STREET: 1455 Pennsylvania Avenue, N.W.  
 CITY: Washington  
 STATE: D.C.  
 ZIP: 20004  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/440,391  
 FILING DATE: 12-MAY-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: WIXON, HENRY N.  
 REGISTRATION NUMBER: 32,073  
 REFERENCE/DOCKET NUMBER: 104322.147  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-942-8400  
 TELEFAX: 202-942-8484  
 INFORMATION FOR SEQ ID NO: 14:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 36 base pairs  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-440-391-14  
 Query Match Similarity 100.0%; Score 102; DB 1; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-10; Mismatches 0; Indels 0; Gaps 0;  
 Matches 20; Conservative 0;  
 Qy 1 TMGQVGRQLAIGDDINRY 20  
 Db 6 TMGQVGRQLAIGDDINRY 25  
 RESULT 12  
 US-08-908-597A-14  
 Sequence 14, Application US/08/908,597A  
 Patent No. 5863795  
 GENERAL INFORMATION:  
 APPLICANT: CHITTENDEN, Thomas D.; and  
 LUTZ, Robert J.  
 TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH  
 MODULATE APOPTOSIS  
 NUMBER OF SEQUENCES: 34  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Hale and Dorr  
 STREET: 1455 Pennsylvania Avenue, N.W.  
 CITY: Washington  
 STATE: D.C.  
 ZIP: 20004  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/236,385A  
 FILING DATE: 25-Jan-1999  
 CLASSIFICATION: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: WIXON, HENRY N.  
 REGISTRATION NUMBER: 32,073  
 (C) ATTORNEY DOCKET NO. 104322.147CIP  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-942-8400  
 TELEFAX: 202-942-8484  
 INFORMATION FOR SEQ ID NO: 14:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 36 base pairs  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
 US-09-236-385A-14

Query Match 100.0%; Score 102; DB 3; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-10;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 14  
 PCT-US96-06122-14  
 Sequence 14, Application PC/TUS9606122  
 GENERAL INFORMATION:  
 APPLICANT: IMMUNOGEN, INC.  
 TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS  
 NUMBER OF SEQUENCES: 34  
 CORRESPONDENCE ADDRESS:  
 STREET: Hale and Dorr  
 STREET: 1455 Pennsylvania Avenue, N.W.  
 CITY: Washington on  
 STATE: D.C.  
 ZIP: 20004  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US96/06122  
 FILING DATE: HERENTH  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/440,391  
 FILING DATE: 12-MAY-1995  
 CLASSIFICATION:  
 REGISTRATION NUMBER: 32,073  
 REFERENCE/DOCKET NUMBER: 104322.147PCT  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-942-8400  
 TELEFAX: 202-942-8484  
 INFORMATION FOR SEQ ID NO: 14:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 36 base pairs  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide  
 PCT-US96-06122-14

Query Match 100.0%; Score 102; DB 5; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-10;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 15  
 US-08-471-058-22  
 Sequence 22, Application US/08471058  
 Patent No. 5770443  
 GENERAL INFORMATION:  
 APPLICANT: Kiefer, Michael C.  
 TITLE OF INVENTION: NOVEL APOPTOSIS MODULATING PROTEINS AND METHODS OF USE  
 NUMBER OF SEQUENCES: 24  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER  
 STREET: 755 PAGE MILL ROAD  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94304-1018  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/471,058  
 FILING DATE: 06-JUN-1995  
 CLASSIFICATION: 800  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/320,157  
 FILING DATE: 07-OCT-1994  
 APPLICATION NUMBER: 08/160,067  
 FILING DATE: 30-NOV-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Lehnhardt, Susan K.  
 REGISTRATION NUMBER: 33,943  
 REFERENCE/DOCKET NUMBER: 23647-20007.12  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-813-5600  
 TELEFAX: 415-494-0792  
 INFORMATION FOR SEQ ID NO: 22:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 152 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-471-058-22

Query Match 100.0%; Score 102; DB 1; Length 152;  
 Best Local Similarity 100.0%; Pred. No. 8.2e-10;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TMGQYGRQLAIGDDINRY 20  
 Db 11 TMGQYGRQLAIGDDINRY 30

RESULT 16  
 US-08-471-057-22  
 Sequence 22, Application US/08471057  
 Patent No. 6015687  
 GENERAL INFORMATION:  
 APPLICANT: Kiefer, Michael C.  
 TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA  
 NUMBER OF SEQUENCES: 22  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: MORRISON & FOERSTER  
 STREET: 755 Page Mill Road  
 CITY: Palo Alto  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94304-1018  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/471,057  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/320,157

FILING DATE: 07-OCT-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: LEHNHARDT, SUSAN K.  
 REFERENCE DOCKET NUMBER: 33,943  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 813-5600  
 TELEFAX: (415) 494-0792  
 TELEX: 706141  
 INFORMATION FOR SEQ ID NO: 22:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 210 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-471-057-22

Query Match 100.0%; Score 102; DB 3; Length 210;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-09;  
 Matches 20; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Qy 1 TMGQVRQLAIGDDINRY 20  
 Db 70 TMGQVRQLAIGDDINRY 89

RESULT 18  
 US-08-321-071A-16  
 / Sequence 16, Application US/08321071A  
 / Patent No. 5672636  
 / GENERAL INFORMATION:  
 / APPLICANT: CHITTENDEN, Thomas D.  
 / TITLE OF INVENTION: APOPTOSIS RELATED PROTEIN BC1-Y, AND METHODS  
 / TITLE OF INVENTION: OF USE THEREOF  
 / NUMBER OF SEQUENCES: 31  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSEE: Hale and Dorr  
 / STREET: 1455 Pennsylvania Avenue, N.W.  
 / CITY: Washington  
 / STATE: D.C.  
 / ZIP: 20004  
 / COMPUTER READABLE FORM:  
 / MEDIUM TYPE: Floppy disk  
 / COMPUTER: IBM PC compatible  
 / OPERATING SYSTEM: PC-DOS/MS-DOS  
 / SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 / APPLICATION NUMBER: US/08/321,071A  
 / FILING DATE: 11-OCT-1994  
 / CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 / APPLICATION NUMBER: PCT/US95/10103  
 / FILING DATE: 09-AUG-1995  
 / PRIOR APPLICATION DATA:  
 / APPLICATION NUMBER: 08/287,427  
 / FILING DATE: 09-AUG-1994  
 / ATTORNEY/AGENT INFORMATION:  
 / NAME: WIXON, HENRY N.  
 / REGISTRATION NUMBER: 32,073  
 / REFERENCE/DOCKET NUMBER: 104322.121C1P  
 / TELECOMMUNICATION INFORMATION:  
 / TELEPHONE: 202-942-8484  
 / TELEFAX: 202-942-8484  
 / INFORMATION FOR SEQ ID NO: 16:  
 / SEQUENCE CHARACTERISTICS:  
 / LENGTH: 211 amino acids  
 / TYPE: amino acid  
 / STRANDEDNESS: single  
 / TOPOLOGY: linear  
 / MOLECULE TYPE: peptide  
 US-08-321-071A-16

Query Match 100.0%; Score 102; DB 1; Length 211;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-09;  
 Matches 20; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Qy 1 TMGQVRQLAIGDDINRY 20  
 Db 70 TMGQVRQLAIGDDINRY 89

RESULT 19  
 US-08-471-058-7  
 / Sequence 7, Application US/08471058  
 / Patent No. 5770443  
 / GENERAL INFORMATION:  
 / APPLICANT: Keifer, Michael C.  
 / TITLE OF INVENTION: NOVEL APOPTOSIS MODULATING  
 / PROTEINS, DNA ENCODING THE PROTEINS AND METHODS OF USE  
 / TITLE OF INVENTION: THEREOF  
 / NUMBER OF SEQUENCES: 24

Query Match 100.0%; Score 102; DB 4; Length 210;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-09;

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: MORRISON & FOERSTER  
 STREET: 755 PAGE MILL ROAD  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94304-1018  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/471,058  
 FILING DATE: 06-JUN-1995  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/320157  
 FILING DATE: 07-OCT-1994  
 APPLICATION NUMBER: 08/160,067  
 FILING DATE: 30-NOV-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Lehnhardt, Susan K.  
 REGISTRATION NUMBER: 33,943  
 REFERENCE/DOCKET NUMBER: 23647-20007.12  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-813-5600  
 TELEX: 415-494-0792  
 TELEFAX: 415-494-0792  
 FILING DATE: 30-NOV-1994  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US/08/471,058  
 FILING DATE: 06-JUN-1995  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/320157  
 FILING DATE: 07-OCT-1994  
 APPLICATION NUMBER: 08/160,067  
 FILING DATE: 30-NOV-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Lehnhardt, Susan K.  
 REGISTRATION NUMBER: 33,943  
 REFERENCE/DOCKET NUMBER: 23647-20007.12  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-813-5600  
 TELEX: 415-494-0792  
 TELEFAX: 415-494-0792  
 LENGTH: 211 amino acids  
 SEQUENCE CHARACTERISTICS:  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: Internal  
 US-08-471-058-9

RESULT 21  
 US-08-471-058-10  
 Sequence 10, Application US/08471058  
 Patent No. 5770443  
 GENERAL INFORMATION:  
 APPLICANT: Kiefer, Michael C.  
 ATTORNEY/AGENT: Barr, Philip J.  
 TITLE OF INVENTION: NOVEL APOPTOSIS MODULATING PROTEINS, DNA ENCODING THE PROTEINS AND METHODS OF USE  
 NUMBER OF SEQUENCES: 24  
 TITLE OF INVENTION: THEREOF  
 NUMBER OF SEQUENCES: 24  
 CORRESPONDENCE ADDRESS:  
 ADDRESSSEE: MORRISON & FOERSTER  
 STREET: 755 PAGE MILL ROAD  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94304-1018  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/471,058  
 FILING DATE: 06-JUN-1995  
 CLASIFICATION: 800  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/320,157  
 FILING DATE: 07-OCT-1994  
 APPLICATION NUMBER: 08/160,067  
 FILING DATE: 30-NOV-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Lehnhardt, Susan K.  
 REGISTRATION NUMBER: 33,943  
 REFERENCE/DOCKET NUMBER: 23647-20007.12  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-813-5600  
 TELEX: 415-494-0792  
 TELEFAX: 415-494-0792

RESULT 20  
 US-08-471-058-9  
 Sequence 9, Application US/08471058  
 Patent No. 5770443  
 GENERAL INFORMATION:  
 APPLICANT: Kiefer, Michael C.  
 ATTORNEY/AGENT: Barr, Philip J.  
 TITLE OF INVENTION: NOVEL APOPTOSIS MODULATING PROTEINS, DNA ENCODING THE PROTEINS AND METHODS OF USE  
 NUMBER OF SEQUENCES: 24  
 CORRESPONDENCE ADDRESS:  
 ADDRESSSEE: MORRISON & FOERSTER  
 STREET: 755 PAGE MILL ROAD  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94304-1018  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/471,058  
 FILING DATE: 06-JUN-1995  
 CLASIFICATION: 800  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/320,157  
 FILING DATE: 07-OCT-1994  
 APPLICATION NUMBER: 08/160,067  
 FILING DATE: 30-NOV-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Lehnhardt, Susan K.  
 REGISTRATION NUMBER: 33,943  
 REFERENCE/DOCKET NUMBER: 23647-20007.12  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-813-5600  
 TELEX: 415-494-0792  
 TELEFAX: 415-494-0792

TELEX: 706141  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 211 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-471-058-10

Query Match 100.0%; Score 102; DB 1; Length 211;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TMGQVGRQLATIGDDINRY 20  
 Db 70 TMGQVGRQLATIGDDINRY 89

RESULT 22  
 US-08-471-058-11  
 Sequence 11, Application US/08471058  
 GENERAL INFORMATION:  
 APPLICANT: Kiefer, Michael C.  
 TITLE OF INVENTION: NOVEL APOPTOSIS MODULATING PROTEINS AND METHODS OF USE  
 NUMBER OF SEQUENCES: 24  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: MORRISON & FOERSTER  
 STREET: 755 Page Mill Road  
 CITY: Palo Alto  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94304-1018

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/944,530  
 FILING DATE: 07-OCT-1997  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/426,529  
 FILING DATE: 20-APR-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Lehnhardt, Susan K.  
 REGISTRATION NUMBER: 33,943  
 REFERENCE/DOCKET NUMBER: 23647-20007.21  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 813-5600  
 TELEFAX: (415) 494-0792  
 TELEX: 706141

INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 211 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

US-08-944-530-2

Query Match 100.0%; Score 102; DB 2; Length 211;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TMGQVGRQLATIGDDINRY 20  
 Db 70 TMGQVGRQLATIGDDINRY 89

RESULT 24  
 US-08-944-530-4  
 Sequence 4, Application US/08944530  
 Patent No. 5998111  
 GENERAL INFORMATION:  
 APPLICANT: BARR, PHILIP J.  
 TITLE OF INVENTION: METHODS OF SCREENING FOR THERAPEUTIC  
 NUMBER OF SEQUENCES: 4  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: MORRISON & FOERSTER  
 STREET: 755 Page Mill Road  
 CITY: Palo Alto  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94304-1018

Query Match 100.0%; Score 102; DB 1; Length 211;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TMGQVGRQLATIGDDINRY 20  
 Db 70 TMGQVGRQLATIGDDINRY 89

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/944,530  
 FILING DATE: 07-OCT-1997  
 PRIORITY APPLICATION DATA:  
 CLASSIFICATION: 435  
 APPLICATION NUMBER: US/08/426,529  
 FILING DATE: 20-APR-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: LEINHARDT, SUSAN K.  
 REGISTRATION NUMBER: 33,943  
 REFERENCE/DOCKET NUMBER: 23647-20007.21  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 813-5600  
 TELEFAX: (415) 494-0792  
 TELEX: 706141  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 211 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-944-530-4

Query Match 100.0%; Score 102; DB 2; L  
 Best Local Similarity 100.0%; Pred. No. 1.2e-09;  
 Matches 20; Conservative 0; Mismatches 0;

Qy	1	20
	TMGQYGRQLAIGDIDNRY	TMGQYGRQLAIGDIDNRY
Db	70	89

RESULT 25  
 US-08-471-057-7  
 Sequence 7, Application US/08471057  
 ; Patent No. 6015687  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KIEFER, MICHAEL C.  
 ; BAER, PHILIP J.  
 ; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PEPTIDES  
 ; TITLE OF INVENTION: ENCODING THE PROTEINS AND METHODS  
 ; NUMBER OF SEQUENCES: 22  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEES: MORRISON & FOERSTER  
 ; STREET: 755 Page Mill Road  
 ; CITY: Palo Alto  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94104-1018  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/471,057  
 FILING DATE:  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/320,157  
 FILING DATE: 07-OCT-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: LEINHARDT, SUSAN K.  
 REGISTRATION NUMBER: 33,943  
 REFERENCE/DOCKET NUMBER: 23647-20007.20  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 813-5600  
 TELEFAX: (415) 494-0792

```

TELEX: 706141
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-471-057-7

RESULT 26
US-08-471-057-9
Query Match 100.0%; Score 102; DB 3; Length 211;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; GENERAL INFORMATION:
; PATENT NO. 6015687
; APPLICANT: KIEFER, MICHAEL C.
; ATTORNEY/AGENT INFORMATION:
; NAME: LISHNHAUT, SUSAN K.
; ADDRESS: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,057
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/320,157
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: LISHNHAUT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5560
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-471-057-9

RESULT 26
US-08-471-057-9
Query Match 100.0%; Score 102; DB 3; Length 211;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; GENERAL INFORMATION:
; PATENT NO. 6015687
; APPLICANT: KIEFER, MICHAEL C.
; ATTORNEY/AGENT INFORMATION:
; NAME: LISHNHAUT, SUSAN K.
; ADDRESS: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,057
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/320,157
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: LISHNHAUT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5560
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-471-057-9

```

US -08-471-057-10  
 ; Sequence 10, Application US/08471057  
 ; Patent No. 6015687  
 GENERAL INFORMATION:  
 APPLICANT: KIEFER, MICHAEL C.  
 APPLICANT: BARR, PHILIP J.  
 TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA  
 TITLE OF INVENTION: ENCODING THE PROTEINS AND METHODS OF USE THEREOF  
 NUMBER OF SEQUENCES: 22  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: MORRISON & FOERSTER  
 STREET: 755 Page Mill Road  
 CITY: Palo Alto  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94304-1018  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/471, 057  
 FILING DATE:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/320, 157  
 FILING DATE: 07-OCT-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: LEHNHARDT, SUSAN K.  
 REGISTRATION NUMBER: 33, 943  
 REFERENCE/DOCKET NUMBER: 23647-20007.20  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 813-5600  
 TELEFAX: (415) 494-0792  
 TELEX: 706141  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 211 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US -08-471-057-10

Query Match 100.0%; Score 102; DB 3; Length 211;  
 Best Local Similarity 100.0%; Pred. No. 1.26-09; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TMGQYGRQLAIGDDINRY 20  
 Db 70 TMGQYGRQLAIGDDINRY 89

RESULT 28  
 US -08-471-057-11  
 ; Sequence 11, Application US/08471057  
 ; Patent No. 6015687  
 GENERAL INFORMATION:  
 APPLICANT: KIEFER, MICHAEL C.  
 APPLICANT: BARR, PHILIP J.  
 TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA  
 TITLE OF INVENTION: ENCODING THE PROTEINS AND METHODS OF USE THEREOF  
 NUMBER OF SEQUENCES: 22  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: MORRISON & FOERSTER  
 STREET: 755 Page Mill Road  
 CITY: Palo Alto  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94304-1018  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/471, 057  
 FILING DATE:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/320, 157  
 FILING DATE: 07-OCT-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: LEHNHARDT, SUSAN K.  
 REGISTRATION NUMBER: 33, 943  
 REFERENCE/DOCKET NUMBER: 23647-20007.20  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 813-5600  
 TELEFAX: (415) 494-0792  
 TELEX: 706141  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 211 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US -08-471-057-11

Query Match 100.0%; Score 102; DB 3; Length 211;  
 Best Local Similarity 100.0%; Pred. No. 1.26-09; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TMGQYGRQLAIGDDINRY 20  
 Db 70 TMGQYGRQLAIGDDINRY 89

RESULT 29  
 US -08-381-488-2  
 ; Sequence 2, Application US/09381488  
 ; Patent No. 6441135  
 ; GENERAL INFORMATION:  
 Qy 1 TMGQYGRQLAIGDDINRY 20  
 Db 70 TMGQYGRQLAIGDDINRY 89

TITLE OF INVENTION: A NOVEL BAK BINDING PROTEIN, DNA  
 NUMBER OF SEQUENCES 7  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: BROWN, THERESA A.  
 STREET: 1560 Broadway, Suite 1200  
 CITY: Denver  
 STATE: CO  
 COUNTRY: USA  
 ZIP: 80202  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/381, 488  
 FILING DATE: 11-Feb-2000  
 CLASSIFICATION: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BROWN, THERESA A.  
 REGISTRATION NUMBER: 32, 547  
 REFERENCE/DOCKET NUMBER: 4147-15-PIUS  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (303) 863-9700  
 TELEFAX: (303) 863-0223  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 211 amino acids  
 TYPE: amino acid

TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 US-09-381-488-2

Query Match 100.0%; Score 102; DB 4; Length 211;  
 Best Local Similarity 100.0%; Prod. No. 1.2e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TMGQYGRQLAIGDDINRY 20  
 Db 70 TMGQYGRQLAIGDDINRY 89

---

RESULT 30  
 / Sequence 7, Application US/08470865  
 / Patent No. 6586395  
 / GENERAL INFORMATION:  
 / APPLICANT: KIEFER, MICHAEL C.  
 / TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA  
 / TITLE OF INVENTION: ENCODING THE PROTEINS AND METHODS OF USE THEREOF  
 / NUMBER OF SEQUENCES: 22  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSEE: MORRISON & FOERSTER  
 / STREET: 755 Page Mill Road  
 / CITY: Palo Alto  
 / STATE: California  
 / COUNTRY: USA  
 / ZIP: 94104-1018  
 / COMPUTER READABLE FORM:  
 / MEDIUM TYPE: Floppy disk  
 / COMPUTER: IBM PC compatible  
 / OPERATING SYSTEM: PC-DOS/MS-DOS  
 / SOFTWARE: PatentIn Release #1.0, Version #1.30  
 / CURRENT APPLICATION DATA:  
 / APPLICATION NUMBER: US/08/470,865  
 / FILING DATE: 06-JUN-1995  
 / CLASIFICATION: 530  
 / PRIORITY APPLICATION DATA:  
 / APPLICATION NUMBER: US 08/320,157  
 / FILING DATE: 07-OCT-1994  
 / ATTORNEY/AGENT INFORMATION:  
 / NAME: LEINHARDT, SUSAN K.  
 / REGISTRATION NUMBER: 33,943  
 / REFERENCE/DOCKET NUMBER: 23647-20007.20  
 / TELECOMMUNICATION INFORMATION:  
 / TELEPHONE: (415) 813-5600  
 / TELEFAX: (415) 494-0790  
 / TELEX: 706141  
 / INFORMATION FOR SEQ ID NO: 9:  
 / SEQUENCE CHARACTERISTICS:  
 / LENGTH: 211 amino acids  
 / TYPE: amino acid  
 / TOPOLOGY: linear  
 / MOLECULE TYPE: protein  
 / US-08-470-865-9

Query Match 100.0%; Score 102; DB 4; Length 211;  
 Best Local Similarity 100.0%; Prod. No. 1.2e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TMGQYGRQLAIGDDINRY 20  
 Db 70 TMGQYGRQLAIGDDINRY 89

---

RESULT 32  
 / Sequence 10, Application US/08470865  
 / Patent No. 6586395  
 / GENERAL INFORMATION:  
 / APPLICANT: KIEFER, MICHAEL C.  
 / APPLICANT: BARR, PHILIP J.  
 / TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA  
 / TITLE OF INVENTION: ENCODING THE PROTEINS AND METHODS OF USE THEREOF  
 / NUMBER OF SEQUENCES: 22  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSEE: MORRISON & FOERSTER  
 / STREET: 755 Page Mill Road  
 / CITY: Palo Alto  
 / STATE: California  
 / COUNTRY: USA  
 / ZIP: 94104-1018  
 / COMPUTER READABLE FORM:  
 / MEDIUM TYPE: Floppy disk  
 / COMPUTER: IBM PC compatible  
 / OPERATING SYSTEM: PC-DOS/MS-DOS  
 / SOFTWARE: PatentIn Release #1.0, Version #1.30  
 / CURRENT APPLICATION DATA:  
 / APPLICATION NUMBER: US/08/470,865

RESULT 31  
 / Sequence 9, Application US/08470865  
 / Patent No. 6586395  
 / GENERAL INFORMATION:

FILING DATE: 06-JUN-1995  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 FILING DATE: 07-OCT-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: LEHNHARDT, SUSAN K.  
 REGISTRATION NUMBER: 33,943  
 REFERENCE/DOCKET NUMBER: 23647-20007.20  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 813-5600  
 TELEFAX: (415) 494-0792  
 TELEX: 706141  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 211 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-470-865-10

Query Match 100.0%; Score 102; DB 4; Length 211;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TMGQYGRQLATIGDDINRY 20  
 Db 70 TMGQYGRQLATIGDDINRY 89

RESULT 34  
 US-09-155-327G-13  
 / Sequence 13, Application US/09155327G  
 / Patent No. 6790637

GENERAL INFORMATION:  
 / APPLICANT: AMRAD Operations Pte Ltd  
 / TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2  
 / FAMILY OF APOPOPTOSIS-CONTROLLING GENES  
 / FILE REFERENCE: 2096584  
 / CURRENT APPLICATION NUMBER: US/09/155,327G  
 / PRIORITY FILING DATE: 1995-03-29  
 / PRIOR APPLICATION NUMBER: PNB965  
 / PRIOR FILING DATE: 1996-03-27  
 / NUMBER OF SEQ ID NOS: 15  
 / SOFTWARE: PatentIn Ver. 2.1  
 / SEQ ID NO 13  
 / LENGTH: 211  
 / TYPE: PRT  
 / ORGANISM: Homo sapiens

US-09-155-327G-13

Query Match 100.0%; Score 102; DB 4; Length 211;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TMGQYGRQLATIGDDINRY 20  
 Db 70 TMGQYGRQLATIGDDINRY 89

RESULT 33  
 US-08-470-865-11  
 / Sequence 11, Application US/08470865

GENERAL INFORMATION:  
 / APPLICANT: KIEFER, MICHAEL C.  
 / APPLICANT: BARR, PHILIP J.  
 / TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA  
 / TITLE OF INVENTION: ENCODING THE PROTEINS AND METHODS OF USE THEREOF  
 / NUMBER OF SEQUENCES: 22  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSEE: MORRISON & FOERSTER  
 / STREET: 755 Page Mill Road  
 / CITY: Palo Alto  
 / STATE: California  
 / COUNTRY: USA  
 / ZIP: 94304-1018

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/470,865  
 FILING DATE: 06-JUN-1995  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/320,157  
 FILING DATE: 07-OCT-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: LEHNHARDT, SUSAN K.  
 REGISTRATION NUMBER: 33,943  
 REFERENCE/DOCKET NUMBER: 23647-20007.20  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 813-5600  
 TELEFAX: (415) 494-0792  
 TELEX: 706141  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 211 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear

US-08-470-865-11  
 / Sequence 11, Application US/08470865

Query Match 100.0%; Score 102; DB 4; Length 211;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TMGQYGRQLATIGDDINRY 20  
 Db 70 TMGQYGRQLATIGDDINRY 89

Search completed: January 26, 2005, 00:52:16  
 Job time : 39 secs

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Om protein - protein search, using bw model

Run on: January 25, 2005, 10:06:02 ; Search time 24.5 Seconds  
(without alignments)  
78.544 Million cell updates/sec

Title: US-09-828-870-36

Perfect score: 102

Sequence: 1 TMGQVRQLATIGDDINRRY 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79;\*  
1: P1r1;\*  
2: p1r2;\*  
3: p1r3;\*  
4: P1r4;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	102	100.0	211	2 S58873	Bak protein - human
2	102	100.0	211	2 S58875	cdd-2 protein - human
3	48	47.1	1329	2 T33136	hypothetical protein
4	46.5	45.6	357	2 T06308	protein phosphatase
5	46	45.1	244	2 G82418	transcription regulator
6	46	45.1	747	2 C75545	phosphotriboyliform
7	46	45.1	833	2 AE0564	H <sub>2</sub> K <sub>+</sub> -exchanging A
8	46	45.1	834	1 C64779	probable copper-tr
9	46	45.1	834	2 E85546	probable ATPase yb
10	46	45.1	834	2 A90696	Cu(I)-translocatio
11	46	45.1	915	2 H82104	cation transport A
12	46	45.1	1226	2 S44824	P58F2.1 protein -
13	45.5	44.6	532	2 JN0084	phytoene dehydroge
14	45	44.1	426	2 S58684	phosphopyruvate hy
15	45	44.1	426	2 H71967	enolase - Helicobac
16	44.5	43.6	774	2 JC7265	terrilysin (EC 3.4
17	44	43.1	234	2 AC3205	ISS66 family Orf4 (
18	44	43.1	258	2 H75027	sy v-atape proteo
19	44	43.1	261	2 B71213	probable chemoce
20	44	43.1	465	2 T48374	UDPG glucosyltrans
21	44	43.1	521	2 T34482	hypothetical prote
22	44	43.1	593	2 S75352	ABC-type transport
23	44	43.1	693	2 G82618	plus biogenesis P
24	44	43.1	803	1 B70041	probable copper-tr
25	43.5	42.6	355	2 H84643	probable protein P
26	43	42.2	65	2 G75258	Conserved hypothetical
27	43	42.2	248	2 T4822	protein - human
28	43	42.2	356	2 S71460	C;Species: Homo sapiens (man)
29	43	42.2	356	2 A533433	C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004

#### ALIGNMENTS

RESULT 1

S58873 Bak protein - human

N;Alternate name: bc1-2 homolog; cdn-1 protein

C;Species: Homo sapiens (man)

C;Accession: S58873; S58876 #sequence\_revision 01-Mar-1996 #text\_change 09-Jul-2004

R;Chittenden, T.; Harrington, E.A.; O' Connor, R.; Flemington, C.; Lutz, R.J.; Evan, G.I.

Nature 374, 733-736, 1995

A;Title: Induction of apoptosis by the bc1-2 homologue Bak.

A;Reference number: S58873; PMID:95231653;

A;Accession: S58873

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-211 <C>H>

A;Cross-references: ENB:184213; NID:9804984; PIDN:CAA585971; PID:9804985

R;Kieff, M.C.; Brauer, M.J.; Powers, V.C.; Wu, J.; Umanbsky, S.R.; Tomei, L.D.; Barr, N.; Parrow, S.N.; White, J.H.M.; Martinou, I.; Raven, T.; Pun, K.T.; Grinham, C.J.; Martin, J.

Nature 374, 731-733, 1995

A;Title: Cloning of a bc1-2 homologue by interaction with adenovirus E1B 19K.

A;Reference number: S58872; PMID:7715731

A;Accession: S58872

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-211 <FAR>

A;Cross-references: UNIPROT:Q16611; EMBL:U23765; NID:9758797; PIDN:AAA93066.1; PID:g758797

A;Title: Modulation of apoptosis by the widely distributed bc1-2 homologue Bak.

A;Reference number: S58874; PMID:95231654; PMID:7715731

A;Accession: S58874

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-211 <KIR>

A;Cross-references: EMBL:U16811; NID:9595923; PIDN:AAA74466.1; PID:9595924

A;Gene: GDB:BAK

A;Cross-references: GDB:635887

Query Match 100.0%; Score 102; DB 2; Length 211;

Best Local Similarity 100.0%; Pred. No. 4.3e-09;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TMGGYGRQIAIGDIDNRY 20

Db 70 TMGGYGRQIAIGDIDNRY 89

RESULT 2

S58875 cdn-2 protein - human

C;Species: Homo sapiens (man)

C;Date: 15-Feb-1996 #sequence\_revision 01-Mar-1996 #text\_change 09-Jul-2004

C;Accession: S58875  
 R;Kiefer, M.C.; Brauer, M.J.; Powers, V.C.; Wu, J.J.; Umansky, S.R.; Tomei, L.D.; Barr, Nature 374, 736-739, 1995  
 A;Title: Modulation of apoptosis by the widely distributed Bcl-2 homologue Bak.  
 A;Reference number: S58874; MUID:95231654; PMID:715731  
 A;Accession: S58875  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Cross-references: UNIPROT:Q13014; EMBL:U16812; PIDN:AAA74467.1; PID:G5959  
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1994

Query Match Similarity 100.0%; Score 102; DB 2; Length 211;  
 Best Local Similarity 100.0%; Pred. No. 4; 3e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 TMGQVGRGOLAIIGDDINRY 20  
 Db 70 TMGQVGRGOLAIIGDDINRY 89

RESULT 3  
 T33136 hypothetical protein C45G7.6 - *Caenorhabditis elegans*  
 C;Species: *Caenorhabditis elegans*  
 C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
 C;Accession: T33136  
 R;Dante, M.; Wamley, P.  
 submitted to the EMBL Data Library, May 1998  
 A;Description: The sequence of C. elegans cosmid C45G7.  
 A;Reference number: 221288  
 A;Molecule type: DNA  
 A;Accession: T33136  
 A;Status: preliminary; translated from GB/EMBL/DBBJ  
 A;Cross-references: UNIPROT:076356; EMBL:AE067611; PIDN:AC19194.1; GSPDB:GN00022; CBSP:  
 A;Experimental source: strain Bristol N2; clone C45G7  
 C;Genetics:  
 A;Map position: 4  
 A;Introns: 27/3; 70/3; 110/3; 356/1; 544/2; 649/3; 750/2; 846/3; 1021/3; 1064/3; 1247/3  
 Query Match Similarity 47.1%; Score 48; DB 2; Length 1329;  
 Best Local Similarity 50.0%; Pred. No. 23;  
 Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;  
 Qy 1 TMGQVGRGOLAIIGDDINRY 20  
 Db 526 TICQVQDSLIIKICGNQRKF 545

RESULT 4  
 T06308 protein phosphatase 2C homolog F11C18.60 - *Arabidopsis thaliana*  
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)  
 C;Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 09-Jul-2004  
 C;Accession: T06308  
 R;Bevan, M.; Terry, N.; Ardiles, W.; Buijschaert, C.; Dasseville, R.; De Clerck, R.; De  
 ewes, H.W.; Mayer, K.F.X.; Schueler, C.  
 submitted to the Protein Sequence Database, April 1999  
 A;Accession number: 215589  
 A;Reference number: T06308  
 A;Molecule type: DNA  
 A;Status: preliminary; BEV>  
 A;Cross-references: UNIPROT:Q9S253; EMBL:AL049607; GSPDB:GN00062; ATSP:F11C18.60  
 A;Experimental source: cultivar Columbia; BAC clone F11C18  
 C;Genetics:  
 A;Gene: ATSP:F11C18.60  
 A;Residues: 1-357  
 A;Map position: 4  
 A;Introns: 39/3; 61/1; 97/2;  
 A;Superfamily: human phosphoprotein phosphatase 1A  
 C;Superfamily: human phosphoprotein phosphatase 1A  
 Query Match Similarity 45.6%; Score 46.5; DB 2; Length 357;

RESULT 6  
 75545  
 phosphoribosylformylglycaminidine synthase II - Deinococcus radiodurans (strain R1)  
 ; Species: Deinococcus radiodurans  
 ; Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
 ; Accession: C75545  
 ; White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.L. Shan, M.; VanAheyan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; J. Smith, H.O.; Venter, J.C.; Fraser, C.M.  
 ; Science 286, 1571-1577, 1999

## RESULT

H<sup>+</sup>/K<sup>+</sup>-exchanging ATPase (EC 3.6.3.10) - *Salmonella enterica* subsp. *enterica* serovar *Typhi*  
 C;Species: *Salmonella enterica* subsp. *enterica* serovar *Typhi*  
 C;Note: this species has also been called *Salmonella typhi*  
 C;Accession: AE0564  
 C;Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, Th. T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O Gaora, P.  
*Nature* 413, 848-852, 2001  
 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skeleton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar A;Reference number: AB0502; MUID:2153497; PMID:11677608  
 A;Accession: AE0564  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-833 <PAR>  
 A;Cross-references: GB:AU513382; PIDN:CAD04983.1; PID:916501768; GSPPDB:GN00176  
 C;Genetics:  
 A;Gene: STY0544  
 C;Superfamily: Bacillus probable copper-transporting ATPase yvgX; ATPase nucleotide-bind  
 C;Keywords: hydrolase

Query Match 45.1%; Score 46; DB 2; Length 833;  
 Best Local Similarity 66.7%; Pred. No. 29;  
 Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GROQAIIGDDIN 17  
 Db 711 GROQAMVGDGIN 722

RESULT 8  
 C64779  
 C;Species: *Escherichia coli* (strain K-12)  
 C;Accession: C64779  
 R;Blacter, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co .A.; Rose, D.J.; Mau, B.; Shao, Y.  
*Science* 277, 1453-1462, 1997  
 A;Title: The complete genome sequence of *Escherichia coli* K-12.  
 A;Reference number: A64720; MUID:9278503  
 A;Accession: C64779  
 A;Status: nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-834 <BLAT>  
 A;Cross-references: UNIPROT:059385; GB:AE000154; GB:U00096; PID:91786681; GSPPDB:GN00096  
 A;Experimental source: strain K-12; substrate MG1655  
 C;Genetics:  
 A;Gene: ybar  
 C;Superfamily: Bacillus probable copper-transporting ATPase yvgX; ATPase nucleotide-bind  
 C;Keywords: ATP; copper binding; hydrolase; ion transport; metal binding; phosphoprotein  
 P;9-38/Domain: heavy-metal-associated homology <HMA1>  
 P;105-134/Domain: heavy-metal-associated homology <HMA2>  
 P;189-205/Domain: transmembrane #status predicted <TM1>  
 P;218-234/Domain: transmembrane #status predicted <TM2>  
 P;224-568/Domain: ATPase transduction domain homology <ATT>  
 P;438-454/Domain: transmembrane #status predicted <TM3>  
 P;468-484/Domain: transmembrane #status predicted <TM4>  
 P;631-647/Domain: transmembrane #status predicted <TM5>  
 P;806-822/Domain: transmembrane #status predicted <TM6>  
 P;108,110,113/Binding site: copper (Mer, Cys) #status predicted  
 P;523/Active site: Asp (aspartylphosphate intermediate) #status predicted

Query Match 45.1%; Score 46; DB 1; Length 834;  
 Best Local Similarity 66.7%; Pred. No. 29;  
 Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GROQAIIGDDIN 17  
 Db 712 GROQAMVGDGIN 723

RESULT 11  
 H8104  
 C;Species: *Vibrio cholerae* (strain N1696)  
 C;Accession: H8104  
 R;Heidelberg, J.P.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. ;Judson, D.; Brinkac, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragot, I.; Sellers, L.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
*Nature* 406, 477-483, 2000  
 A;Title: DNA sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.  
 A;Reference number: A82035; MUID:20406833

A;Accession: H82104  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-915 <HEI>  
 A;Cross-references: UNIPROT:Q9K277; GB:AE004293; NID:99656766; PIDN:AAF9535  
 A;Experimental source: serogroup O1; strain N16961; biotype El Tor  
 C;Genetics:  
 A;Gene: VC2215  
 A;Map position: 1  
 C;Superfamily: Bacillus probable copper-transporting ATPase yvgX; ATPase nucleotide-bind  
 Query Match 45.1%; Score 46; DB 2; Length 915;  
 Best Local Similarity 64.3%; Pred. No. 32;  
 Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 QY 4 QVGROLAIIQGDIN 17  
 DB 786 QVGKVKVAMIGDGIN 799

RESULT 12  
 S44324  
 P5412.1 protein - *Caenorhabditis elegans*  
 C;Date: 14-Sep-1994 #sequence\_revision 12-May-1995 #text\_change 09-Jul-2004  
 C;Accession: S44824  
 R;Anderson, K  
 Submitted to the EMBL Data Library, September 1993  
 A;Description: Sequence of the *C. elegans* cosmid F54F2.  
 A;Accession: S44824  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-1226 <AND>  
 A;Cross-references: UNIPROT:P34446; EMBL:L23645; NID:9388603; PID:9388605  
 C;Genetics:  
 A;Introns: 59/2; 137/3; 179/1; 316/2; 393/1; 551/3; 597/2; 662/2; 899/3; 1178/3  
 C;Keywords: cytoskeleton; transmembrane protein

Query Match 45.1%; Score 46; DB 2; Length 1226;  
 Best Local Similarity 53.8%; Pred. No. 44;  
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
 QY 3 QVGROLAIIQGD 15  
 DB 359 GVGKVKVAMIGDGDD 371

RESULT 13  
 JN0084  
 Phycoene dehydrogenase (EC 1.3.1.1) - *Aphanocapsa* sp. (PCC 6714)  
 N;Alternate names: phycoene desaturase  
 C;Species: *Aphanocapsa* sp.  
 C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 09-Jul-2004  
 C;Accession: JN0084  
 R;Schmidt, A.; Sandmann, G.  
 Gene 91, 113-117, 1990  
 A;Title: Cloning and nucleotide sequence of the crtI gene encoding phytoene dehydrogenase  
 A;Reference number: JN0084; MUID:90382685; PMID:2119326  
 A;Accession: JN0084  
 A;Molecule type: DNA  
 A;Residues: 1-1332 <SCH>  
 A;Cross-references: UNIPROT:P21134; GB:MF5647; GB:MF3237; NID:9141989; PIDN:AAA62573.1;  
 A;Note: the authors translated the codon CAG for residue 380 as Gly  
 C;Comment: This enzyme catalyzes the symmetrical introduction of two double bonds at C-1  
 C;Genetics:  
 A;Gene: crtI  
 C;Superfamily: carotenoid biosynthesis; membrane bound; oxidoreductase  
 C;Keywords: carotenoid biosynthesis; membrane bound; oxidoreductase

Query Match 44.6%; Score 45.5; DB 2; Length 532;  
 Best Local Similarity 42.9%; Pred. No. 21;  
 Matches 9; Conservative 7; Mismatches 2; Indels 3; Gaps 1;

QY 2 MGQVGROLAI---IGGDINRR 19  
 Db 140 IGQTRQLQLEFIGEDVHRQ 160

RESULT 14  
 S58684  
 phosphopyruvate hydratase (EC 4.2.1.11) - *Helicobacter pylori* (strains 26695 and others)  
 N;Alternate names: enolase  
 C;Species: *Helicobacter pylori*  
 C;Date: 29-Nov-1995 #sequence\_revision 17-Sep-1997 #text\_change 09-Jul-2004  
 C;Accession: B64539; S58684  
 R;Tomb, J.P.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenna, N.; Kelley, J.M.; Cottrell, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.; Nature 388, 539-547, 1997  
 A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karp, P.D.; Smith, H.O.; Fraser, C.;Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.  
 A;Reference number: A64520; MUID:97394467; PMID:9252185  
 A;Accession: B64539  
 A;Status: nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-426 <TOM>  
 A;Cross-references: UNIPROT:P49285; GB:AE000536; NID:92313230; PIDN:AAD072:  
 R;Schmitt, W.; Odembreit, S.; Heuermann, D.; Haas, R.  
 A;Experimental source: strain 26695  
 A;Cross-references: UNIPROT:P49285; GB:AE000536; NID:92313230; PIDN:AAD072:  
 R;Schmitt, W.; Odembreit, S.; Heuermann, D.; Haas, R.  
 A;Gene: HP0154  
 C;Cross-references: UNIPROT:P49285; GB:AE000536; NID:92313230; PIDN:AAD072:  
 C;Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase; magnesium  
 P;12/Binding site: magnesium 2 (Ser) #status predicted  
 F;205/338/Active site: Glu, Lys #status predicted  
 F;242,286,313/Binding site: magnesium 1 (Asp, Glu, Asp) #status predicted  
 A;Accession: S58684  
 A;Molecule type: DNA  
 A;Residues: 1-25; 'I', 27-68 <SCH>  
 A;Cross-references: EMBL:235478  
 C;Genetics:  
 C;Function:  
 A;Description: catalyzes the reversible dehydration of 2-phospho-D-glyceric acid to phot  
 A;Pathway: glycolysis  
 C;Superfamily: enolase  
 C;Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase; magnesium  
 P;12/Binding site: magnesium 2 (Ser) #status predicted  
 F;205/338/Active site: Glu, Lys #status predicted  
 F;242,286,313/Binding site: magnesium 1 (Asp, Glu, Asp) #status predicted  
 Query Match 44.1%; Score 45; DB 2; Length 426;  
 Best Local Similarity 46.2%; Pred. No. 20;  
 Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;  
 QY 4 QVGROLAIIQGD 16  
 Db 303 ELCRQIQVQGDD 315

RESULT 15  
 H71967  
 enolase - *Helicobacter pylori* (strain J99)  
 C;Variety: strain J99  
 C;Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 09-Jul-2004  
 C;Accession: H71967  
 R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.B.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Mertz, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999  
 A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric pathi  
 A;Reference number: A71800; MUID:99120557; PMID:9923682  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-426 <ARN>  
 A;Cross-references: UNIPROT:Q9ZNS6; GB:AE001453; NID:94154651; PIDN:AAD0572:  
 A;Experimental source: strain J99  
 C;Genetics:

A;Gene: eno  
C;Superfamily: enolase  
Query Match 44.1%; Score 45; DB 2; Length 426;  
Best Local Similarity 46.2%; Pred. No. 20;  
Matches 6; Conservative 1; Mismatches 0;  
Matches 6; Conservat 1; Mismatches 0;  
Indels 0; Gaps 0;  
QY 4 QVGROLAIIIGDDI 16  
::|||: ::|||:  
DB 303 ELGRQIQLVcDDL 315

Search completed: January 25, 2005, 10:27:39  
Job time : 26.5 secs

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Scoring table:	BLOSUM62		ALIGNMENTS	
Searched:	1825181 seqs, 575374646 residues			
Total number of hits satisfying chosen parameters:	1825181			
Minimum DB seq length:	0			
Maximum DB seq length:	2000000000			
Post-processing:	Minimum Match 0%			
	Maximum Match 100%			
Database :	UniProt 02: 1: uniprot_sprot;* 2: uniprot_trembl;*			
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
SUMMARIES				
Result No.	Score	Query	Match	Length
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2	102	100.0	190	2
3	102	100.0	211	1
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5	101	100.0	211	1
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7	92	90.2	151	2
8	92	90.2	151	2
9	92	90.2	208	1
10	92	90.2	209	2
11	92	90.2	209	2
12	50	49.0	264	2
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14	50	49.0	264	2
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19	47	46.1	265	2
20	47	46.1	373	2
21	47	46.1	1430	2
22	46.5	45.6	357	2
23	46	45.1	244	2
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288

Submitted (MAR-2003) to the EMBL/GenBank/DDbj databases.  
[5]

Submitted (MAR-2003) to the EMBL/GenBank/DDJB databases.	
[5] N N	SEQUENCE FROM N.A.
SEQUENCE FROM N.A.	MEDLINE=22935763; PubMed=14574404; DOI=10.1038/nature02055;
Mungall A.J., Palmer S.A., Sims S.K., Edwards C.A., Ashurst J.L., Wilming L., Jones M.C., Horton R., Hunt S.E., Scott C.E., Gilbert J.G.R., Clamp M.B., Bethel G., Milne S., Ainscough R., ABBADIE J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S., Babbage A.K., Bagguley C.D., Bailey J., Banerjee R., Barker D.J., Barlow K.F., Bates K., Beare D.M., Beasley H., Besley C., Bird C.P., Blaikie S.E., Bray-Alien S., Brook J., Brown J.Y., Burford D.C., Burrill W., Burton J., Carter C., Carter N.P., Chapman J.C., Clark S.Y., Clark G., Clegg C.M., Cobley V., Collier R.E., Collins J.B., Colman I.K., Corby N.R., Coville G.J., Culley K.M., Dhami P., Davies J., Dunn M., Earthrow M.E., Ellington A.E., Evans K.A., Faulkner L., Francis M.D., Frankish A., Franklin J., French L., Garner P., Garnett J., Ghori M.J., Gill L.M., Gillison C.J., Glithero R.J., Grainger D.V., Grant M., Gribble S., Griffiths C., Griffiths M.N.D., Hall R., Hallis K.S., Hammonds S.J., Hart J.B., Hart E.A., Heath P.D., Heathcote R., Holmes S.J., Howden P.J., Howe K.L., Howell G.R., Hucke E., Humphrey S.J., Humphries M.D., Hunt A.R., Johnson C.M., Joy A.A., Kay M., Keenan S.J., Kimberley A., King A., Laird G.K., Langford C., Lawlor S., Leongamornlert D.A., Leverhulme M., Lloyd D.M., Loveland J.B., Lovell J., Martin S., Mashreghi-Mohammadi M., Mathews L., Matthews L., McCann O.T., McLaren S.J., McIay K., McMurray A., Moore M.J.F., Mullikin J.C., Nickerson T., Novik K.L., Oliver K., Overton-Larby E.K., Parker A., Patel R., Pearce A.V., Peck A.I., Phillippe B.J.C.T., Phillips S., Plumb R.W., Porter K.M., Ramsey Y., Ranby S.A., Rice C.M., Ross M.T., Seale S.M., Sehra H.K., Sheridan B., Skuce C.D., Smith S., Smith M., Spraggan L., Squares S.L., Stewart C.A., Sycamore N., Tamlyn-Hall G., Tester J., Theaker A.J., Thomas D.W., Thorpe A., Tracey A., Tromans A., Tubby B., Wall M., Wallis J.M., West A.P., White S.S., Whithead S.L., Whittaker H., Wild A., Willey D.J., Wilmer T.E., Wood J.M., Wray P.W., Wyatt J.C., Young I., Younger R.M., Younger D.R., Coullon A., Durbin R., Hubbard T., Sulston J.B., Dunham I., Rogers J., Beck S., Nature 425:805-811(2003).]	
[6] N N	SEQUENCE FROM N.A.
SEQUENCE FROM N.A.	TISSUE-LUNG;
C C	MEDLINE=22388557; PubMed=12477932; DOI=10.1073/pnas.242603899;
A A	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collin F.S., Wagner J., Shemesh C.M., Schuler G.D., Altschul S.F., Zeeberg B., Bustow K.H., Schaefer C.P., Bhat N.K., Hopkins R.F., Jordon H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Petrus G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villanueva D.K., Muzzy D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J.J., Heitman E., Ketteman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnierch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[7] N N	SEQUENCE OF 96-2006 FROM N.A.
A A	"Estrogen alters expression of apoptosis-regulators, Bcl-2, Bcl-xL and Bak, as well as susceptibility to therapeutic agents of human breast cancer cells"; Submitted (NOV-1996) to the EMBL/GenBank/DDJB databases.
P P	MUTAGENESIS, AND FUNCTION OF BH3 DOMAIN; MEDLINE=96091131; PubMed=8521816;
T T	STRUCTURE BY NMR OF 72-87; MEDLINE=97172562; PubMed=9020082;
R A	"A conserved domain in Bak, distinct from BH1 and BH2, mediates cell death and protein binding functions.;" Sattler M., Liang H., Netterheim D., Meadow R.P., Harlan J.E., Thompson C.B., Fesik S.W.; RT
R A	STRUCTURE OF Bcl-xL-Bak peptide complex: recognition between repressor Bcl-2 or its adenovirus homolog E1B 19k protein. RT
R A	STRUCTURE OF Bcl-2, E1B 19k protein, and Bcl-xL. RT
R A	SUBUNIT: Forms heterodimers with Bcl-2, E1B 19k protein, and Bcl-xL.
R A	SUBCELLULAR LOCATION: Membrane-bound (Potential).
R A	TISSUE SPECIFICITY: Expressed in a wide variety of tissues, with highest levels in the heart and skeletal muscle.
R A	DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD and BAX for their proapoptotic activity and for their interaction with anti-apoptotic members of the Bcl-1-2 family.
R A	SIMILARITY: Belongs to the Bcl-2 family.
R A	SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
R A	SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
R A	SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
R A	STRUCTURE-PROTEIN entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation in the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announcement">http://www.isb-sib.ch/announcement</a> or send an email to license@isb-sib.ch).
R A	DR EMBL; X82121; CAI58997.1; DR EMBL; U23765; AAA93006.1; DR EMBL; U16811; AAA74466.1; DR EMBL; UY260471; AA0756298.1; DR EMBL; 293017; CAB05626.1; DR EMBL; BC004431; AAH04431.1; DR EMBL; BC004431; AAH04431.1; DR EMBL; D88397; BAA13606.1; DR EMBL; D88396; BAA13606.1; DR PRR; S58873; S58873; DR PDB; 1BXL; PDB; B7-87. DR EMBL; HGNC:949; BAK1. DR MM; 600516; DR GO; GO:0008837; P:apoptotic mitochondrial changes; TAS. DR PROSITE; PS00662; BCL2_FAMILY; 1. DR InterPro; IPR000712; BCL2_BH. DR InterPro; IPR002475; BCL2_FAMILY. DR PIA; PPI042; BCL2; 1. DR PROSITE; PS00662; BCL2_FAMILY; 1. DR PROSITE; PS01080; BH1; 1. DR PROSITE; PS01158; BH2; 1. DR PROSITE; PS01259; BH3; 1. KW 3D-structure: Apoptosis; Polymorphism; Transmembrane. DR DOMAIN; 74 88 BH3. DR DOMAIN; 117 136 BH1. DR DOMAIN; 169 184 BH2. DR VARIANT; 188 205 Potential. DR VARIANT; 28 28 A->V. /PRId=VAR_018829. S->R. /PRId=VAR_018830.
S Q	SEQUENCE 211 AA; 23409 MW; A2200FF72A46D04 CRC64; 100.0% score 102; DB 1; Length 211; Query Match



Qy	2 MGQVGRQLAITGDDINRY 20	STRAIN=Swiss; TISSUE=Liver;
Db	69 LGQVGRQLAITGDDINRY 87	PUBMED=9299236;
RESULT 8		
AAH57589	AAH57589; PRELIMINARY; PRT; 151 AA.	
AC	AAH57589; PRELIMINARY; PRT; 151 AA.	
DT	02-MAR-2004 (TrEMBLrel. 27, Created)	
DT	02-MAR-2004 (TrEMBLrel. 27, Last sequence update)	
DT	02-MAR-2004 (TrEMBLrel. 27, Last annotation update)	
DE	Bak1 protein.	
OS	Mus musculus (Mouse).	
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OC	NCBI_TaxID=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=CS7BL/6; TISSUE=Brain;	
RX	MEDLINE=23388257; PubMed=12477932;	
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins P.S., Wagner L., Shearmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Moresina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.O., Mullahy S.J., Bosak S.A., McFarlan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimes J.W., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Shalska U., Smallius D.E., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=CS7BL/6; TISSUE=Brain;	
RA	Strausberg R.; Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.	
DR	EMBL:BC057589; AAH157589.1; -	
SQ	SEQUENCE 151 AA; 18C13BPF86E4F33B CRC64;	
Query	2 MGQVGRQLAITGDDINRY 20	Match 90.2%; Score 92; DB 2; Length 151;
Match	Best Local Similarity 89.5%; Pred. No. 3.6e-06;	Match 90.2%; Score 92; DB 1; Length 208;
Match	Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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RESULT 9		
BAK_MOUSE	STANDARD; PRT; 208 AA.	
ID	008734; PRELIMINARY; PRT; 208 AA.	
AC	008734; PRELIMINARY; PRT; 208 AA.	
DT	01-NOV-1997 (Rel. 35, Created)	
DT	01-NOV-1997 (Rel. 35, Last sequence update)	
DT	05-JUL-2004 (Rel. 44, Last annotation update)	
DB	Bcl-2 homologous antagonist/killer (Apoptosis regulator BAK).	
GN	Name=Bak1; Synonyms=Bak;	
OS	Mus musculus (Mouse).	
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OC	NCBI_TaxID=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RESULT 10		
08C264	Q8C264; PRELIMINARY; PRT; 209 AA.	
ID	Q8C264; PRELIMINARY; PRT; 209 AA.	
AC	Q8C264; PRELIMINARY; PRT; 209 AA.	
DT	01-MAR-2003 (TrEMBLrel. 23, Created)	
DT	01-MAR-2003 (TrEMBLrel. 23, Last sequence update)	
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)	
DE	Mus musculus NOD-derived CD1c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F630041J23 product:BCL2-antagonist/killer 1, full insert sequence.	
GN	Name=Bak1;	
OS	Mus musculus (Mouse).	
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OC	NCBI_TaxID=10090;	
OX		

[1]	RN SEQUENCE FROM N.A. STRAIN=NOD;	Query Match 90.2%; Score 92; DB 2; Length 209; Best Local Similarity 89.5%; Pred. No. 4.9e-06; Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
[2]	RX MEDLINE=9279253; PubMed=10349636; Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44 (1999).	Query 2 MGQYGRQLAIGDDINRRY 20 Db 69 LGQYGRQLAIGDDINRRY 87
[3]	RN SEQUENCE FROM N.A. STRAIN=NOD;	RESULT 11 Q9JK59 PRELIMINARY; PRT; 209 AA. ID Q9JK59 AC Q9JK59 DT 01-OCT-2000 (TREMBLrel. 15, Created) DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update) DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
[4]	RN SEQUENCE FROM N.A. STRAIN=NOD; RA THE FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I & II Team; RA "Analysis of the mouse transcriptome based on functional annotation of RT 60,770 full-length cDNAs."; RT Nature 420:563-573 (2002).	RA Name=Bak; Rattus norvegicus (Rat). Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. NCBI_TaxID=10116; RN [1] RN RP SEQUENCE FROM N.A. RC STRAIN=Sprague-Dawley; RX MEDLINE=22672518; PubMed=12787069; RA Itoh T., Itoh A.; Pleasure D.; RT "Bcl-2-related protein family gene expression during oligodendroglial differentiation"; RL J. Neurochem. 85:1500-1512 (2003). DR EMBL; AP259504; AF071760.1; DR HSSP; Q16611; 1BXL. DR GO:0042931; Pregulation of apoptosis; IEA. DR InterPro; IPR00712; Bcl2_BH. DR InterPro; IPR002475; Bcl2_Family. PFAM; PF00452; Bcl-2; 1. DR SMART; SM00337; BCL1; 1. DR PROSITE; PS50062; BCL2_FAMILY; 1. DR PROSITE; PS01080; BH1; UNKNOWN_1. DR PROSITE; PS01258; BH2; 1. DR PROSITE; PS01259; BH3; 1. SQ SEQUENCE 209 AA; 23:153 MW; 2493B814B1972421 CRC64;
[5]	RN SEQUENCE FROM N.A. STRAIN=NOD;	Query Match 90.2%; Score 92; DB 2; Length 209; Best Local Similarity 89.5%; Pred. No. 4.9e-06; Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
[6]	RX MEDLINE=20530913; PubMed=11076681; RA Shiba K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P., RA Konno H., Akiyama J., Nishi K., Kitasuna H., Tashiro H., Hayashizaki Y., RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishio T., Harada A., RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., RA Fujiwara S., Inoue K., Togawa Y., Iwasa M., Ohara B., Watahiki M., RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka K., Matsunura S., Kawai J., RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; RT "RIKEN integrated sequence analysis (RISA) system-84-format sequencing pipeline with 384 multicapillary sequencer."; RT Genome Res. 10:1757-1771(2000).	RESULT 12 Q74116 Q74116 PRELIMINARY; PRT; 264 AA. ID Q74116; Q6SEB1. AC AC DT DT 05-JUL-2004 (TREMBLrel. 27, Created) DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update) DT 01-OCT-2004 (TREMBLrel. 28, Last annotation update)
[7]	RN SEQUENCE FROM N.A. STRAIN=NOD;	DE Hypothetical protein. GN OrderedCucusName=w1752; ORFNNames=Ljo_1752; OS Lactobacillus johnsonii NCC 533. OC Lactobacillus, Firmicutes; Lactobacillales; Lactobacillaceae; NCBI_TaxID=257314; RN [1] RP SEQUENCE FROM N.A. RC STRAIN=NCC 533; RA Published=14966310; Berger B., Desiere F., Vilanova D., Barretto C., Pridmore R.D., Berger B., Desiere F., Vilanova D., Barretto C., RA Pittet A.-C., Zwahlen M.-C., Rouvet M., Altermann E., Barrangou R., RA Moller B., Mercenier A., Klaenhammer T., Arigoni F., Scheff M.A.; RT "The genome sequence of the probiotic intestinal bacterium

RT Lactobacillus johnsonii NCC 533.";	OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
RL Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517 (2004).	OC Lactobacillus.
RN [2]	NCBI TaxID=31959;
RP SEQUENCE FROM N.A.	RN [1]
RC STRAIN=NCC 533;	RP SEQUENCE FROM N.A.
RX Published=15016546;	RC STRAIN=NCC 533;
RA Ventura M., Canchaya C., Pridmore R.D., Brussow H.;	RA PubMed=14966510;
RT "The prophages of Lactobacillus johnsonii NCC 533: comparative	RA Pridmore R.D., Berger B., Desiere F., Vilanova D., Barretto C., Barrangou R.,
RT Genomics and transposition analysis.";	RA Pillet A.-C., Zwahlen M.-C., Rouvet M., Altermann E., Scheill M.A.;
RT Virology 320:229-242 (2004).	RA Mallet B., Mercenier A., Klaenhammer T., Arigoni F., Scheill M.A.;
RL EMBL; AE017705; AAS09524.; -.	RT "The genome sequence of the probiotic intestinal bacterium
DR EMBL; AY59534; AAR27400.1.; -.	RT Lactobacillus johnsonii. NCC 533.";
DR InterPro: IPR003593; AAA ATPase.	RL Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517 (2004).
DR InterPro: IPR001543; PTSK_SPOIIIE.	DR EMBL; AB017205; AAS0954.1.; -.
DR Pfam: PF01580; FtsK_SpoIIIE.	KW Hypothetical protein.
DR SMART: SM00382; AAA_1.	DR EMBL; AB016940; AAS0954.1.; -.
DR PROSITE; PS50501; FTSK; 1.	KW Hypothetical protein.
KW ATP-binding.	SQ SEQUENCE 264 AA; 29627 MW; 0066E4D619E84367 CRC64;
Query Match 49.0%; Score 50; DB 2; Length 264;	Query Match 49.0%; Score 50; DB 2; Length 264;
Best Local Similarity 45.0%; Pred. No. 21;	Best Local Similarity 45.0%; Pred. No. 21;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0; Gaps 0;	Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
QY 1 TMGQYGRQLAIGDDINRY 20	QY 1 TMGQYGRQLAIGDDINRY 20
Db 79 TTNQIARMRLINENNANNRY 98	Db 79 TTNQIARMRLINENNANNRY 98
RESULT 15	RESULT 15
K6P3_BACTN	K6P3_BACTN
ID K6P3_BACTN	ID K6P3_BACTN
STRAIN=NPI-582 / ATCC 29148;	STRAIN=NPI-582 / ATCC 29148;
AC Q842E9;	AC Q842E9;
DT 10-OCT-2003 (Rel. 42, Created)	DT 10-OCT-2003 (Rel. 42, Created)
DR 05-OCT-2003 (Rel. 42, Last sequence update)	DR 05-OCT-2004 (Rel. 44, Last sequence update)
DR 05-JUL-2004 (Rel. 44, Last annotation update)	DR 05-JUL-2004 (Rel. 44, Last annotation update)
DB 6-phosphofructokinase 3 (EC 2.7.1.11) (Phosphofructokinase 3)	DB 6-phosphofructokinase 3 (EC 2.7.1.11) (Phosphofructokinase 3)
GN Name=pfKA3; OrderedLocusNames=BT1356;	GN Name=pfKA3; OrderedLocusNames=BT1356;
OS Bacteroides thetaiotomicron.	OS Bacteroides thetaiotomicron.
CA Bacteroides; Bacteroidetes; Bacteroides (class); Bacteroidales;	CA Bacteroides; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.	OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;	OX NCBI_TaxID=818;
RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.
RC MEDLINE=22550858; PubMed=1263928; DOI=10.1126/science.1080029;	RC MEDLINE=22550858; PubMed=1263928; DOI=10.1126/science.1080029;
RA Xu J., Bjurzell M.K., Fimrod J., Deng S., Carmichael L.K.,	RA Xu J., Bjurzell M.K., Fimrod J., Deng S., Carmichael L.K.,
RA Chiang H.C., Hooper L.V., Gordon J.I.,	RA Chiang H.C., Hooper L.V., Gordon J.I.,
RT "A genomic view of the human-Bacteroides thetaiotomicron symbiosis.";	RT "A genomic view of the human-Bacteroides thetaiotomicron symbiosis.";
RT Science 299:2074-2076 (2003).	RT Science 299:2074-2076 (2003).
CC -I- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-	CC -I- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-
CC fructose 1,6-bisphosphate.	CC fructose 1,6-bisphosphate.
CC -I- PATHWAY: Key control step of glycolysis.	CC -I- PATHWAY: Key control step of glycolysis.
CC -I- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).	CC -I- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -I- SIMILARITY: Belongs to the phosphofructokinase Family.	CC -I- SIMILARITY: Belongs to the phosphofructokinase Family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration	CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -	CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its	CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial	CC entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>
CC or send an email to license@isb-sib.ch).	CC or send an email to license@isb-sib.ch).
DR EMBL; AB016940; AA078432.1; -.	DR EMBL; AB016940; AA078432.1; -.
DR HSSP; P06998; 2PFK.	DR HSSP; P06998; 2PFK.
DR HAMAP; MF_00339; -; 1.	DR HAMAP; MF_00339; -; 1.
DR InterPro; IPR000023; PfFructokinase.	DR InterPro; IPR000023; PfFructokinase.
DR Pfam; PF00365; PFK.	DR Pfam; PF00365; PFK.
DR PRINTS; PR00476; PfFructokinase.	DR PRINTS; PR00476; PfFructokinase.
DR ProDom; PD000707; PfFructokinase.	DR ProDom; PD000707; PfFructokinase.
DR PROSITE; PS00433; PHOSPHOFRUCTOKINASE; FALSE NEG.	DR PROSITE; PS00433; PHOSPHOFRUCTOKINASE; FALSE NEG.
DR Allosteric enzyme; ATP-binding; Complete proteome; Glycolysis; Kinase;	DR Allosteric enzyme; ATP-binding; Complete proteome; Glycolysis; Kinase;
KW Magnesium; Transferase.	KW Magnesium; Transferase.
OS NP_BIND	OS NP_BIND
FT ATP (By similarity).	FT ATP (By similarity).

PT NP BIND 160 164 ATP (By similarity).  
PT NP BIND 177 193 ATP (By similarity).  
PT ACT SITE 133 133 Proton acceptor (By similarity).  
PT BINDING 168 168 Substrate (By similarity).  
PT BINDING 255 255 Substrate (By similarity).  
PT BINDING 264 264 Substrate (By similarity).  
SQ SEQUENCEB 336 AA: 35853 MW; 990BAEF6B5BDF79 CRC64;  
Query Match 48.0%; Score 49; DB 1; Length 336;  
Best Local Similarity 60.0%; Pred. No. 39;  
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
Qy 3 GOVERQLAIGDDIN 17  
| | | | : | | | :  
Db 290 GOVERQLAIGDDIN 304

Search completed: January 25, 2005, 10:10:33  
Job time : 134 secs

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OM protein - protein search, using SW model

Run on: January 25, 2005, 10:06:01 ; Search time 28 Seconds  
(without alignments)

47.370 Million cell updates/sec

Title: US-09-828-870-39  
Perfect score: 104  
Sequence: 1 AADPLHEAMRAAGDBEFETRF 20

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*

2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*

3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*

4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*

5: /cgn2\_6/ptodata/1/iaa/PECTUS\_COMB.pep:\*

6: /cgn2\_6/ptodata/1/iaa/backfiles.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	104	100.0	20	3 US-09-236-385A-39	Sequence 39, Appl
2	101	97.1	27	4 US-09-544-664B-24	Sequence 24, Appl
3	101	97.1	192	1 US-09-798-897-5	Sequence 5, Appl
4	101	97.1	192	1 US-09-798-897-6	Sequence 6, Appl
5	101	97.1	192	2 US-09-978-523-5	Sequence 5, Appl
6	101	97.1	192	2 US-09-978-523-6	Sequence 6, Appl
7	101	97.1	193	1 US-08-798-897-3	Sequence 3, Appl
8	101	97.1	193	1 US-08-798-897-4	Sequence 4, Appl
9	101	97.1	193	2 US-08-978-523-3	Sequence 3, Appl
10	101	97.1	193	2 US-08-978-523-4	Sequence 4, Appl
11	101	97.1	193	4 US-09-155-327G-7	Sequence 7, Appl
12	101	97.1	193	4 US-09-155-327G-9	Sequence 9, Appl
13	101	97.1	333	4 US-09-155-327G-10	Sequence 10, Appl
14	101	97.1	333	4 US-09-149-476-696	Sequence 69, Appl
15	101	97.1	365	4 US-09-010-147B-24	Sequence 24, Appl
16	82	78.8	16	4 US-09-544-664B-51	Sequence 51, Appl
17	54	51.9	27	4 US-09-544-664B-12	Sequence 12, Appl
18	54	51.9	190	1 US-08-981-448-2	Sequence 2, Appl
19	54	51.9	190	2 US-08-470-670A-2	Sequence 2, Appl
20	54	51.9	190	3 US-08-461-511A-2	Sequence 2, Appl
21	54	51.9	190	3 US-09-271-014A-2	Sequence 2, Appl
22	54	51.9	190	5 PCT-US94-07089-5	Sequence 2, Appl
23	51	49.0	27	4 US-09-544-664B-13	Sequence 13, Appl
24	51	49.0	49	1 US-08-322-071A-26	Sequence 26, Appl
25	51	49.0	109	3 US-08-470-670A-11	Sequence 11, Appl
26	51	49.0	121	2 US-08-470-670A-15	Sequence 15, Appl

## ALIGNMENTS

RESULT 1  
US-09-236-385A-39  
; Sequence 39, Application US/09236385A  
; Patent No. 6221615  
; GENERAL INFORMATION:  
; APPLICANT: CHITTENDEN, Thomas D.; and  
; LUTZ, Robert J.  
; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH  
; MODULATE APOPTOSIS  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESSE: Hale and Dorr  
; STREET: 1455 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/236,385A  
; FILING DATE: 25-Jun-1999  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WIXON, HENRY N.  
; REGISTRATION NUMBER: 32,073  
; TELECOMMUNICATION INFORMATION:  
; (C) ATTORNEY DOCKET NO. 104322.147CIP  
; TELEPHONE: 202-942-8400  
; TELEFAX: 202-942-8484  
; INFORMATION FOR SEQ ID NO: 39  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 39  
; US-09-236-385A-39  
; Query Match 100.0%; Score 104; DB 3; Length 20;  
; Best Local Similarity 100.0%; Pred. No. 7.4e-11;  
; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
; Qy 1 AADPLHEAMRAAGDBEFETRF 20  
; Db 1 AADPLHEAMRAAGDBEFETRF 20

RESULT 2  
 US-09-544-664B-24  
 ; Sequence 24, Application US/09544664B  
 ; Patent No. 6713280  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Huang, Zweiwei  
 ; APPLICANT: Wang, Jialun  
 ; APPLICANT: Zhang, Zhiqia  
 ; APPLICANT: Shan, Shimai  
 ; APPLICANT: Lu, Zhiqian  
 ; TITLE OF INVENTION: Enhancement of Peptide Cellular Uptake  
 ; CURRENT APPLICATION NUMBER: US/09/544,664B  
 ; PRIORITY APPLICATION NUMBER: PCT/US00/09352  
 ; PRIORITY FILING DATE: 2000-04-06  
 ; PRIORITY FILING DATE: 1999-04-07  
 ; NUMBER OF SEQ ID NOS: 58  
 ; SOFTWARE: Patentin Ver. 2.1  
 ; SEQ ID NO: 24  
 ; LENGTH: 27  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Peptide  
 ; OTHER INFORMATION: Segment from BH3 domain of a Bcl-2 superfamily  
 ; OTHER INFORMATION: Peptidomimetic  
 ; OTHER INFORMATION: polypeptide  
 ; US-09-544-664B-24

Query Match 97.1%; Score 101; DB 4; Length 27;  
 Best Local Similarity 95.0%; Pred. No. 3.e-06;  
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AADPLHEAMRAAGDEDEFTRF 20  
 Db 4 AADPLHQAMRAAGDEDEFTRF 23

RESULT 3  
 US-08-798-897-5  
 ; Sequence 5, Application US/08798897  
 ; Patent No. 5783201  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Guastella, John  
 ; TITLE OF INVENTION: Genes Coding For Bcl-2  
 ; NUMBER OF SEQUENCES: 53  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: SPERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
 ; STREET: 1100 New York Avenue, N.W., Suite 600  
 ; CITY: Washington  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20005  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/798-897  
 ; FILING DATE: February 11, 1997  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Edmund, Robert W.  
 ; REGISTRATION NUMBER: 32,893  
 ; TELECOMMUNICATION INFORMATION:  
 ; REFERENCE DOCKET NUMBER: 1483.0140001  
 ; NAME: Edmund, Robert W.  
 ; REGISTRATION NUMBER: 32,893  
 ; TELEPHONE: 202-371-2600  
 ; TELEFAX: 202-371-2540  
 ; INFORMATION FOR SEQ ID NO: 6:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 192 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: not relevant  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-798-897-6

Query Match 97.1%; Score 101; DB 1; Length 192;  
 Best Local Similarity 95.0%; Pred. No. 3.e-09;  
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AADPLHEAMRAAGDEDEFTRF 20  
 Db 37 AADPLHQAMRAAGDEDEFTRF 56

RESULT 5  
 US-08-978-523-5  
 ; Sequence 5, Application US/08978523  
 ; Patent No. 5833229  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Guastella, John  
 ; TITLE OF INVENTION: Genes Coding For Bcl-2

i TITLE OF INVENTION: Homologue  
 i NUMBER OF SEQUENCES: 53  
 i CORRESPONDENCE ADDRESS:  
 i ADDRESSEE: STEERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
 i STREET: 1100 New York Avenue, N.W., Suite 600  
 i CITY: Washington  
 i STATE: DC  
 i COUNTRY: USA  
 i ZIP: 20005  
 i COMPUTER READABLE FORM:  
 i MEDIUM TYPE: Floppy disk  
 i COMPUTER: IBM PC compatible  
 i OPERATING SYSTEM: PC-DOS/MS-DOS  
 i SOFTWARE: PatentIn Release #1.0, Version #1.30  
 i CURRENT APPLICATION DATA:  
 i APPLICATION NUMBER: US/08/978,523  
 i FILING DATE: herewith  
 i CLASSIFICATION: 424  
 i PRIORITY APPLICATION DATA:  
 i APPLICATION NUMBER: US 08/798,897  
 i FILING DATE: February 11, 1997  
 i CLASSIFICATION: 424  
 i ATTORNEY/AGENT INFORMATION:  
 i NAME: Esmond, Robert W.  
 i REGISTRATION NUMBER: 32,893  
 i REFERENCE/DOCKET NUMBER: 1483.0140002  
 i TELECOMMUNICATION INFORMATION:  
 i TELEPHONE: 202-371-2600  
 i TELEFAX: 202-371-2540  
 i INFORMATION FOR SEQ ID NO: 5:  
 i SEQUENCE CHARACTERISTICS:  
 i LENGTH: 192 amino acids  
 i TYPE: amino acid  
 i STRANDEDNESS: not relevant  
 i TOPOLOGY: linear  
 i MOLECULE TYPE: protein  
 i US-08-978-523-5

Query Match 97.1%; Score 101; DB 2; Length 192;  
 Best Local Similarity 95.0%; Pred. No. 3.1e-09; Indels 0; Gaps 0;

Qy 1 AADPLHEAMRAAGDEFETRF 20  
 Db 37 AADPLHQANRAAGDEFETRF 56

RESULT 6  
 US-08-978-523-6  
 i Sequence 6, Application US/08978523  
 i Patent No. 5883229

i GENERAL INFORMATION:  
 i APPLICANT: Guaestella, John  
 i TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2  
 i TITLE OF INVENTION: Homologue  
 i NUMBER OF SEQUENCES: 53  
 i CORRESPONDENCE ADDRESS:  
 i ADDRESSEE: STEERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
 i STREET: 1100 New York Avenue, N.W., Suite 600  
 i CITY: Washington  
 i STATE: DC  
 i COUNTRY: USA  
 i ZIP: 20005  
 i COMPUTER READABLE FORM:  
 i MEDIUM TYPE: Floppy disk  
 i COMPUTER: IBM PC compatible  
 i OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:  
 i SOFTWARE: PatentIn Release #1.0, Version #1.30  
 i ATTORNEY/AGENT INFORMATION:  
 i NAME: Esmond, Robert W.  
 i REGISTRATION NUMBER: 32,893  
 i REFERENCE/DOCKET NUMBER: 1483.0140001  
 i TELECOMMUNICATION INFORMATION:  
 i TELEPHONE: 202-371-2600  
 i TELEFAX: 202-371-2540  
 i INFORMATION FOR SEQ ID NO: 3:  
 i SEQUENCE CHARACTERISTICS:  
 i LENGTH: 193 amino acids  
 i TYPE: amino acid  
 i STRANDEDNESS: not relevant  
 i TOPOLOGY: linear  
 i MOLECULE TYPE: protein  
 i US-08-978-897-3

Query Match 97.1%; Score 101; DB 1; Length 193;  
 Best Local Similarity 95.0%; Pred. No. 3.1e-09; Indels 0; Gaps 0;



SEQUENCE CHARACTERISTICS:  
 LENGTH: 193 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: not relevant  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-978-523-4

Query Match 97.1%; Score 101; DB 2; Length 193;  
 Best Local Similarity 95.0%; Pred. No. 3.1e-09;  
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 SEQ ID NO: 9  
 Db 38 AADPLHQAMRAAGDEFETRF 57

RESULT 11  
 US-09-155-327G-7  
 ; Sequence 7, Application US/09155327G  
 ; Patent No. 6790637  
 ; GENERAL INFORMATION:  
 ; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2  
 ; CURRENT APPLICATION NUMBER: US/09/155.327G  
 ; FILE REFERENCE: 2096584  
 ; PRIORITY FILING DATE: 1996-03-27  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 7  
 ; LENGTH: 193  
 ; TYPE: PRT  
 ; ORGANISM: HUMAN  
 US-09-155-327G-7

Query Match 97.1%; Score 101; DB 4; Length 193;  
 Best Local Similarity 95.0%; Pred. No. 3.1e-09;  
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 SEQ ID NO: 9  
 Db 38 AADPLHQAMRAAGDEFETRF 57

RESULT 12  
 US-09-155-327G-9  
 ; Sequence 9, Application US/09155327G  
 ; Patent No. 6790637  
 ; GENERAL INFORMATION:  
 ; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2  
 ; CURRENT APPLICATION NUMBER: US/09/155.327G  
 ; FILE REFERENCE: 2096584  
 ; PRIORITY FILING DATE: 1996-03-29  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO: 9  
 ; LENGTH: 193  
 ; TYPE: PRT  
 ; ORGANISM: Mouse  
 US-09-155-327G-9

Query Match 97.1%; Score 101; DB 4; Length 193;  
 Best Local Similarity 95.0%; Pred. No. 3.1e-09;  
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 SEQ ID NO: 9  
 Db 38 AADPLHQAMRAAGDEFETRF 57

RESULT 13  
 US-09-155-327G-10  
 ; Sequence 10, Application US/09155327G  
 ; Patent No. 6790637  
 ; GENERAL INFORMATION:  
 ; APPLICANT: AMRAD Operations Pty Ltd  
 ; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2  
 ; TITLE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES  
 ; FILE REFERENCE: 2096584  
 ; CURRENT APPLICATION NUMBER: US/09/155.327G  
 ; CURRENT FILING DATE: 1999-03-29  
 ; PRIORITY APPLICATION NUMBER: PN8965  
 ; PRIORITY FILING DATE: 1996-03-27  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 10  
 ; LENGTH: 333  
 ; TYPE: PRT  
 ; ORGANISM: murine  
 US-09-155-327G-10

Query Match 97.1%; Score 101; DB 4; Length 333;  
 Best Local Similarity 95.0%; Pred. No. 5.9e-09;  
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 SEQ ID NO: 10  
 Db 38 AADPLHEAMRAAGDEFETRF 20

Query Match 97.1%; Score 101; DB 4; Length 333;  
 Best Local Similarity 95.0%; Pred. No. 5.9e-09;  
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 SEQ ID NO: 11  
 Db 38 AADPLHEAMRAAGDEFETRF 57

RESULT 14  
 US-09-149-476-696  
 ; Sequence 696, Application US/09149476  
 ; Patent No. 6420526  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: 186 Human Secreted proteins  
 ; FILE REFERENCE: PZ002P1  
 ; CURRENT APPLICATION NUMBER: US/09/149,476  
 ; CURRENT FILING DATE: 1998-09-18  
 ; EARLIER APPLICATION NUMBER: PCT/US98/04493  
 ; EARLIER FILING DATE: 1998-03-06  
 ; EARLIER APPLICATION NUMBER: 60/040,162  
 ; EARLIER FILING DATE: 1997-03-07  
 ; EARLIER APPLICATION NUMBER: 60/040,333  
 ; EARLIER FILING DATE: 1997-03-07  
 ; EARLIER APPLICATION NUMBER: 60/038,621  
 ; EARLIER FILING DATE: 1997-03-07  
 ; EARLIER APPLICATION NUMBER: 60/040,626  
 ; EARLIER FILING DATE: 1997-03-07  
 ; EARLIER APPLICATION NUMBER: 60/040,334  
 ; EARLIER FILING DATE: 1997-03-07  
 ; EARLIER APPLICATION NUMBER: 60/038,336  
 ; EARLIER FILING DATE: 1997-03-07  
 ; EARLIER APPLICATION NUMBER: 60/040,163  
 ; EARLIER FILING DATE: 1997-03-07  
 ; EARLIER APPLICATION NUMBER: 60/047,600  
 ; EARLIER FILING DATE: 1997-05-23  
 ; EARLIER APPLICATION NUMBER: 60/047,615  
 ; EARLIER FILING DATE: 1997-05-23  
 ; EARLIER APPLICATION NUMBER: 60/047,597  
 ; EARLIER FILING DATE: 1997-05-23  
 ; EARLIER APPLICATION NUMBER: 60/047,502  
 ; EARLIER FILING DATE: 1997-05-23  
 ; EARLIER APPLICATION NUMBER: 60/047,633  
 ; EARLIER FILING DATE: 1997-05-23  
 ; EARLIER APPLICATION NUMBER: 60/047,583  
 ; EARLIER FILING DATE: 1997-05-23  
 ; EARLIER APPLICATION NUMBER: 60/047,617

EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,618  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,503  
EARLIER FILING DATE: 1997-05-23  
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EARLIER FILING DATE: 1997-05-23  
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EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,492  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,584  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,500  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,587  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,499  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,598  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,613  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,582  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,596  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,612  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,632  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,601  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,580  
EARLIER FILING DATE: 1997-04-11  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,568  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,314  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,569  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,311  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,671  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,674  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,669  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,312  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,313  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,672  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,315  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/048,974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/056,886  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/055,877  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,889  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,893  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,872  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,877

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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match 97.1%; Score 101; DB 4; Length 365;
Best Local Similarity 95.0%; Pred. No. 6.5e-09;
Matches 19; Conservative 1; Mismatches 0;
Indels 0; Gaps 0;

Qy 1 AADPLHEAMRAAGDEFETRF 20
Db 38 AADPLHQAMRAAGDEFETRF 57

Search completed: January 25, 2005, 10:15:36
Job time : 29 secs



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Query Match 97.1%; Score 101; DB 4; Length 365;
Best Local Similarity 95.0%; Pred. No. 6.5e-09;
Matches 19; Conservative 1; Mismatches 0;
Indels 0; Gaps 0;

Qy 1 AADPLHEAMRAAGDEFETRF 20
Db 38 AADPLHQAMRAAGDEFETRF 57

RESULT 15
US-09-010-147B-24
; Sequence 24, Application US/09010147B
; Patent No. 6653445
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Human Proteins
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC
; COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,147B
; FILING DATE: 12-No. 6653445-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,205
; FILING DATE: 21-JAN-1997
; APPLICATION NUMBER: US 60/034,204
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Jonathan L. Klein
; REGISTRATION NUMBER: 41,119
; INFORMATION FOR SEQ ID NO: 24:
; REFERENCE/DOCKET NUMBER: PF153
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; LENGTH: 365 amino acids
; TYPE: amino acid
; TOPOLOGY: Linear
; MOLECULE TYPE: Protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-010-147B-24

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OM protein - protein search, using SW model

Run on: January 25, 2005, 10:10:46 ; Search time 97.5 Seconds  
(without alignments)

74.111 Million cell updates/sec

Title: US-09-828-870-39

Perfect score: 104

Sequence: 1 ADDPHEAMRAAGDDEFETRF 20

Scoring table: BL0SUM62

Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Database : Published Applications AA: \*

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3: /cgn2\_6/ptodata/1/pubpaa/us06\_NEW\_PUB.pep:\*

4: /cgn2\_6/ptodata/1/pubpaa/us06\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*

6: /cgn2\_6/ptodata/1/pubpaa/PCFTUS\_PUBCOMB.pep:\*

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19: /cgn2\_6/ptodata/1/pubpaa/us60\_NEW\_PUB.pep:\*

20: /cgn2\_6/ptodata/1/pubpaa/us60\_PUBCOMB.pep:\*

RESULT 1  
US-09-828-870-39

Sequence 39, Application US-09828870  
Publication No. US2004054129A1

GENERAL INFORMATION:

APPLICANT: CHITTENDEN, Thomas D.; and  
LUTZ, Robert J.

TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH  
MODULATE APOPTOSIS

NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorf  
STREET: 1455 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.

ZIP: 20004

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/828,870  
FILING DATE: 10-Apr-2001  
CLASSIFICATION: Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/236,385  
FILING DATE: 25-JANUARY-1999  
ATTORNEY/AGENT INFORMATION:  
NAME: WIXON, HENRY N.  
REGISTRATION NUMBER: 32,073  
(C) ATTORNEY DOCKET NO 104322.147CIP

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-942-8400  
TELEFAX: 202-942-8484

INFORMATION FOR SEQ ID NO: 39

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	101	97.1	193	9 US-09-925-674A-7	Sequence 7, Appl.
3	101	97.1	193	9 US-09-925-674A-9	Sequence 9, Appl.
4	101	97.1	193	16 US-10-450-366-6	Sequence 6, Appl.
5	101	97.1	365	10 US-09-809-391-696	Sequence 696, Appl.
6	101	97.1	365	10 US-09-882-171-696	Sequence 696, Appl.
7	101	97.1	365	14 US-10-164-861-696	Sequence 696, Appl.
8	74	71.2	15	9 US-09-738-396-16	Sequence 16, Appl.
9	67	64.4	228	16 US-10-659-705-2	Sequence 2, Appl.
10	56	53.8	179	14 US-10-402-017-6	Sequence 8, Appl.
11	56	53.8	199	14 US-10-402-017-8	Sequence 10, Appl.
12	56	53.8	219	14 US-10-402-017-10	Sequence 2, Appl.
13	54	51.9	190	9 US-09-952-278-2	

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SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 39
US-09-828-870-39

Query Match 100.0%; Score 104; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.e-10; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
US-09-925-674A-7
; Sequence 7, Application US/0925674A
; Patent No. US20020119943A1
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2
; TITLE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES
; FILE REFERENCE: 11886a
; CURRENT APPLICATION NUMBER: US/09/925, 674A
; CURRENT FILING DATE: 2001-08-09
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: P/N965
; PRIOR FILING DATE: 1996-03-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 7
; LENGTH: 193
; TYPE: PRT
; ORGANISM: HUMAN
US-09-925-674A-7

Query Match 97.1%; Score 101; DB 9; Length 193;
Best Local Similarity 95.0%; Pred. No. 2.6e-08; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
US-09-925-674A-9
; Sequence 9, Application US/0925674A
; Patent No. US20020119943A1
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2
; TITLE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES
; FILE REFERENCE: 11886a
; CURRENT APPLICATION NUMBER: US/09/925, 674A
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: P/N965
; PRIOR FILING DATE: 1996-03-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 9
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Mouse
US-09-925-674A-9

Query Match 97.1%; Score 101; DB 9; Length 193;
Best Local Similarity 95.0%; Pred. No. 2.6e-08; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
US-10-450-366-6
; Sequence 6, Application US/10450366
; Publication No. US200401566A1
; GENERAL INFORMATION:
; APPLICANT: Tschopp, Jorg
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: DNA-Sequences, Which Code For An Apoptosis Signal Transduction P:
; FILE REFERENCE: 11436*3
; CURRENT APPLICATION NUMBER: US/10/450,366
; PRIOR APPLICATION NUMBER: PCT/EP01/14597
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: DE 100 61 766-2
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: DE 101 00 280-7
; PRIOR FILING DATE: 2001-01-04
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 6
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human Bcl-W
US-10-450-366-6

Query Match 97.1%; Score 101; DB 16; Length 193;
Best Local Similarity 95.0%; Pred. No. 2.6e-08; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
US-09-809-391-696
; Sequence 696, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PAlM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 696
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-809-391-696

Query Match 97.1%; Score 101; DB 10; Length 365;
Best Local Similarity 95.0%; Pred. No. 5.2e-08; Mismatches 0; Indels 0; Gaps 0;

RESULT 6
US-09-809-391-696
; Sequence 696, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PAlM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 696
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-809-391-696

Query Match 97.1%; Score 101; DB 9; Length 193;
Best Local Similarity 95.0%; Pred. No. 2.6e-08; Mismatches 0; Indels 0; Gaps 0;

RESULT 7
US-09-809-391-696
; Sequence 696, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PAlM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 696
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-809-391-696

Query Match 97.1%; Score 101; DB 9; Length 193;
Best Local Similarity 95.0%; Pred. No. 2.6e-08; Mismatches 0; Indels 0; Gaps 0;

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US-09-882-1171-696  
 ; Sequence 656, Application US/09882171  
 ; Publication No. US20030175858A1

GENERAL INFORMATION:  
 APPLICANT: Ruben et al.  
 TITLE OF INVENTION: 186 Human Secreted proteins

FILE REFERENCE: P2002P2

CURRENT APPLICATION NUMBER: US/09/882,171  
 CURRENT FILING DATE: 2001-05-18

PRIOR APPLICATION NUMBER: 09/809,391  
 PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 09/149,476  
 PRIOR FILING DATE: 1998-09-08

PRIOR APPLICATION NUMBER: PCT/US98/04493  
 PRIOR FILING DATE: 1998-03-06

PRIOR APPLICATION NUMBER: 60/040,162  
 PRIOR FILING DATE: 1997-03-07

PRIOR APPLICATION NUMBER: 60/040,333  
 PRIOR FILING DATE: 1997-03-07

PRIOR APPLICATION NUMBER: 60/038,621  
 PRIOR FILING DATE: 1997-03-07

PRIOR APPLICATION NUMBER: 60/040,626  
 PRIOR FILING DATE: 1997-03-07

PRIOR APPLICATION NUMBER: 60/040,334  
 PRIOR FILING DATE: 1997-03-07

PRIOR APPLICATION NUMBER: 60/040,336  
 PRIOR FILING DATE: 1997-03-07

PRIOR APPLICATION NUMBER: 60/040,626  
 PRIOR FILING DATE: 1997-03-07

PRIOR APPLICATION NUMBER: 60/047,600  
 PRIOR FILING DATE: 1997-05-23

PRIOR APPLICATION NUMBER: 60/047,615  
 PRIOR FILING DATE: 1997-05-23

PRIOR APPLICATION NUMBER: 60/047,597  
 PRIOR FILING DATE: 1997-05-23

PRIOR APPLICATION NUMBER: 60/047,502  
 PRIOR FILING DATE: 1997-05-23

PRIOR APPLICATION NUMBER: 60/047,633  
 PRIOR FILING DATE: 1997-05-23

PRIOR APPLICATION NUMBER: 60/047,583  
 PRIOR FILING DATE: 1997-05-23

PRIOR APPLICATION NUMBER: 60/047,617  
 PRIOR FILING DATE: 1997-05-23

PRIOR APPLICATION NUMBER: 60/047,618  
 PRIOR FILING DATE: 1997-05-23

PRIOR APPLICATION NUMBER: 60/047,503  
 PRIOR FILING DATE: 1997-05-23

PRIOR APPLICATION NUMBER: 60/047,592  
 PRIOR FILING DATE: 1997-05-23

PRIOR APPLICATION NUMBER: 60/047,618  
 PRIOR FILING DATE: 1997-05-23

PRIOR APPLICATION NUMBER: 60/047,584  
 PRIOR FILING DATE: 1997-05-23

PRIOR APPLICATION NUMBER: 60/047,598  
 PRIOR FILING DATE: 1997-05-23

PRIOR APPLICATION NUMBER: 60/047,596  
 PRIOR FILING DATE: 1997-05-23

PRIOR APPLICATION NUMBER: 60/047,613  
 PRIOR FILING DATE: 1997-05-23

PRIOR APPLICATION NUMBER: 60/047,492  
 PRIOR FILING DATE: 1997-05-23

PRIOR APPLICATION NUMBER: 60/047,582  
 PRIOR FILING DATE: 1997-05-23

PRIOR APPLICATION NUMBER: 60/047,598  
 PRIOR FILING DATE: 1997-05-23

PRIOR APPLICATION NUMBER: 60/047,612  
 PRIOR FILING DATE: 1997-05-23

PRIOR APPLICATION NUMBER: 60/047,632  
 PRIOR FILING DATE: 1997-05-23

PRIOR APPLICATION NUMBER: 60/047,601  
 PRIOR FILING DATE: 1997-05-23

PRIOR APPLICATION NUMBER: 60/043,580  
 ; PRIOR FILING DATE: 1997-04-11  
 ; PRIOR APPLICATION NUMBER: 60/043,568  
 ; PRIOR FILING DATE: 1997-04-11  
 ; PRIOR APPLICATION NUMBER: 60/043,314  
 ; PRIOR FILING DATE: 1997-04-11  
 ; PRIOR APPLICATION NUMBER: 60/043,569  
 ; PRIOR FILING DATE: 1997-04-11  
 ; PRIOR APPLICATION NUMBER: 60/043,311  
 ; PRIOR FILING DATE: 1997-04-11  
 ; PRIOR APPLICATION NUMBER: 60/043,671  
 ; PRIOR FILING DATE: 1997-04-11  
 ; PRIOR APPLICATION NUMBER: 60/043,674  
 ; PRIOR FILING DATE: 1997-04-11  
 ; PRIOR APPLICATION NUMBER: 60/043,669  
 ; PRIOR FILING DATE: 1997-04-11  
 ; PRIOR APPLICATION NUMBER: 60/043,312  
 ; PRIOR FILING DATE: 1997-04-11  
 ; PRIOR APPLICATION NUMBER: 60/043,313  
 ; PRIOR FILING DATE: 1997-04-11  
 ; PRIOR APPLICATION NUMBER: 60/043,672  
 ; PRIOR FILING DATE: 1997-04-11  
 ; PRIOR APPLICATION NUMBER: 60/043,315  
 ; PRIOR FILING DATE: 1997-04-11  
 ; PRIOR APPLICATION NUMBER: 60/043,313  
 ; PRIOR FILING DATE: 1997-04-11  
 ; PRIOR APPLICATION NUMBER: 60/043,674  
 ; PRIOR FILING DATE: 1997-04-11  
 ; PRIOR APPLICATION NUMBER: 60/043,666  
 ; PRIOR FILING DATE: 1997-04-11  
 ; PRIOR APPLICATION NUMBER: 60/043,315  
 ; PRIOR FILING DATE: 1997-04-11  
 ; PRIOR APPLICATION NUMBER: 60/048,974  
 ; PRIOR FILING DATE: 1997-06-06  
 ; PRIOR APPLICATION NUMBER: 60/043,572  
 ; PRIOR FILING DATE: 1997-04-11  
 ; PRIOR APPLICATION NUMBER: 60/056,886  
 ; PRIOR FILING DATE: 1997-08-22  
 ; PRIOR APPLICATION NUMBER: 60/056,877  
 ; PRIOR FILING DATE: 1997-08-22  
 ; PRIOR APPLICATION NUMBER: 60/056,889  
 ; PRIOR FILING DATE: 1997-08-22  
 ; PRIOR APPLICATION NUMBER: 60/056,893  
 ; PRIOR FILING DATE: 1997-08-22  
 ; PRIOR APPLICATION NUMBER: 60/056,872  
 ; PRIOR FILING DATE: 1997-08-22  
 ; PRIOR APPLICATION NUMBER: 60/056,882  
 ; PRIOR FILING DATE: 1997-08-22  
 ; PRIOR APPLICATION NUMBER: 60/056,881  
 ; PRIOR FILING DATE: 1997-08-22  
 ; PRIOR APPLICATION NUMBER: 60/056,877  
 ; PRIOR FILING DATE: 1997-08-22  
 ; PRIOR APPLICATION NUMBER: 60/056,903  
 ; PRIOR FILING DATE: 1997-08-22  
 ; PRIOR APPLICATION NUMBER: 60/056,888  
 ; PRIOR FILING DATE: 1997-08-22  
 ; PRIOR APPLICATION NUMBER: 60/056,879  
 ; PRIOR FILING DATE: 1997-08-22  
 ; PRIOR APPLICATION NUMBER: 60/056,880  
 ; PRIOR FILING DATE: 1997-08-22  
 ; PRIOR APPLICATION NUMBER: 60/056,874  
 ; PRIOR FILING DATE: 1997-08-22  
 ; PRIOR APPLICATION NUMBER: 60/056,870  
 ; PRIOR FILING DATE: 1997-08-22  
 ; PRIOR APPLICATION NUMBER: 60/056,836  
 ; PRIOR FILING DATE: 1997-08-22  
 ; PRIOR APPLICATION NUMBER: 60/056,864  
 ; PRIOR FILING DATE: 1997-08-22  
 ; PRIOR APPLICATION NUMBER: 60/056,874  
 ; PRIOR FILING DATE: 1997-08-22  
 ; PRIOR APPLICATION NUMBER: 60/056,845  
 ; PRIOR FILING DATE: 1997-08-22  
 ; PRIOR APPLICATION NUMBER: 60/056,892  
 ; PRIOR FILING DATE: 1997-08-22  
 ; PRIOR APPLICATION NUMBER: 60/057,761

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; CURRENT APPLICATION NUMBER: US/10/164,861
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US/09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 757
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 696
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-164-861-696

Query Match 97.1%; Score 101; DB 14; Length 365;
Best Local Similarity 95.0%; Pred. No. 5.2e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AADPLHEAMRAAGDEFETRF 20
Db 38 AADPLHQAMRAAGDEFETRF 57

RESULT 8
US-09-738-396-16
; Sequence 16, Application US/09738396
; Patent No. US20010029013A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; ATTORNEY: Goczik, Adam
; TITLE OF INVENTION: BCL-G Polypeptides, Encoding Nucleic Acids and Methods
; FILE REFERENCE: P-LJ 4450
; CURRENT APPLICATION NUMBER: US/09/738,396
; TITLE OF INVENTION: of Use
; FILE REFERENCE: P-LJ 4450
; CURRENT FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: US 09/461,641
; PRIOR FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 16
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-738-396-16

Query Match 71.2%; Score 74; DB 9; Length 15;
Best Local Similarity 93.3%; Pred. No. 3.9e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LHEAMRAAGDEFETR 19
Db 1 LHQAMRAAGDEFETR 15

RESULT 9
US-10-659-705-2
; Sequence 2, Application US/10659705
; Publication No. US20040117867A1
; GENERAL INFORMATION:
; APPLICANT: Lengenau, David M.
; ATTORNEY: Lengenau, David M.
; TITLE OF INVENTION: Transgenic Cancer Models in Fish
; FILE REFERENCE: 112706-123
; CURRENT APPLICATION NUMBER: US/10/659,705
; CURRENT FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 09/409,585
; PRIOR FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 2
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Artificial Sequence

Query Match 97.1%; Score 101; DB 10; Length 365;
Best Local Similarity 95.0%; Pred. No. 5.2e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AADPLHEAMRAAGDEFETRF 20
Db 38 AADPLHQAMRAAGDEFETRF 57

RESULT 7
US-10-164-861-596
; Sequence 696, Application US/10164861
; Publication No. US2003025246A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, et al.
; ATTORNEY: Rosen, et al.
; TITLE OF INVENTION: 186 Human Secreted Proteins
; FILE REFERENCE: P2002P21
; CURRENT APPLICATION NUMBER: US 09/409,585
; PRIOR FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 2
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Artificial Sequence

```



SEQUENCE CHARACTERISTICS:  
 LENGTH: 190 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: Protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 US-09-952-278-2

Query Match 51.9%; Score 54; DB 9; Length 190;  
 Best Local Similarity 52.6%; Pred. No. 1.;  
 Matches 10; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ADPLHEAMRAAGDEFETRF 20  
 Db 79 ASDVQRQLRDAGDEFELRY 97

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RESULT 14  
 US-10-659-705-7  
 Sequence 7, Application US/10659705  
 Publication No. US20040117867A1  
 GENERAL INFORMATION:  
 APPLICANT: Look, A. Thomas  
 TITLE OF INVENTION: Transgenic Cancer Models in Fish  
 CURRENT APPLICATION NUMBER: US/10/659,705  
 CURRENT FILING DATE: 2003-09-11  
 PRIOR APPLICATION NUMBER: US 60/409,585  
 PRIOR FILING DATE: 2002-09-11  
 NUMBER OF SEQ ID NOS: 8  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 7  
 LENGTH: 229  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: BCL2 proteins  
 US-10-659-705-7

Query Match 51.9%; Score 54; DB 16; Length 229;  
 Best Local Similarity 52.6%; Pred. No. 1.5%;  
 Matches 10; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ADPLHEAMRAAGDEFETRF 20  
 Db 79 ASDVQRQLRDAGDEFELRY 97

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RESULT 15  
 US-10-158-769-2  
 Sequence 2, Application US/10158769  
 Publication No. US20030008924A1  
 GENERAL INFORMATION:  
 APPLICANT: Weng, Shaomeng  
 TITLE OF INVENTION: Small Molecule Antagonists of BCL-2 Family Protein  
 FILE REFERENCE: US-07232  
 CURRENT APPLICATION NUMBER: US/10/158,769  
 CURRENT FILING DATE: 2002-09-09  
 PRIOR APPLICATION NUMBER: 60/293,983  
 NUMBER OF SEQ ID NOS: 3  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 2  
 LENGTH: 152  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Synthetic  
 US-10-158-769-2

Query Match 51.0%; Score 53; DB 14; Length 152;

Result No.	Score	Query Match	Length	DB ID	Description	SUMMARIES	
1	104	100.0	20	5 AAU77894	Aau77894 Bcl-w pep	XX	XX
2	104	100.0	20	8 ADK14726	Adk14726 Bcl-2 rel	PR	PR
3	101	97.1	27	3 AAB37024	Aab37024 Bcl2 poly	XX	XX
4	101	97.1	168	4 AAW36048	AAw36048 Mouse bcl	XX	XX
5	101	97.1	183	8 ADP88350	Adp88350 Derivatival	XX	XX
6	101	97.1	192	2 AAW97394	Aaw97394 Mammalian	XX	XX
7	101	97.1	192	2 AAW97393	Aaw97393 Protein s	XX	XX
8	101	97.1	192	2 AAY05533	Aay05533 Mouse Bcl	PT	PT
9	101	97.1	193	2 AAW36047	AAw36047 Human bcl	PT	PT
10	101	97.1	193	2 AAW61392	AAw61392 Human bcl	XX	XX
11	101	97.1	193	2 AAW1191	AAw1191 Rat bcl-Y	PS	PS
12	101	97.1	193	2 AAW97392	Aaw97392 The human	XX	XX
13	101	97.1	193	2 AAW97391	Aaw97391 The rat b	XX	XX
14	101	97.1	193	2 AAY05530	Aay05530 Human Bcl	CC	CC
15	101	97.1	193	2 AAY05532	Aay05532 Human Bcl	CC	CC
16	101	97.1	193	2 AAY05531	Aay05531 Mouse Bcl	CC	CC
17	101	97.1	193	7 ADD474	Add474 Human Pro	CC	CC
18	101	97.1	193	8 ADD88349	Adp88349 Human Bcl	CC	CC
19	101	97.1	365	2 AAW59884	Aaw59884 Amino aci	CC	CC
20	101	97.1	365	5 ABG95556	Abg95556 Human nov	CC	CC
21	101	97.1	365	6 ABO34750	Abo34750 Fragment	CC	CC
22	101	97.1	365	7 ADT23411	Adt23411 Novel hum	CC	CC
23	101	97.1	365	8 AAB37051	Aab37051 Bcl2 poly	CC	CC
24	82	78.8	16	3 AAB37051	Aab37051 BH3 domai	CC	CC
25	74	71.2	4	4 AAB85177	Aab85177 BH3 ability to block GD domain-mediated interactions	CC	CC

## ALIGNMENTS

RESULT 1  
ID AAU77894 standard; peptide; 20 AA.

AAU77894;  
AC  
XX  
DT 05-JUN-2002 (first entry)  
XX  
DE Bcl-w peptide tested for ability to block GD domain interactions.  
XX  
KW GD domain; apoptosis; interaction with Bcl-XL; cell killing function;  
KW bak; cell death regulatory molecule; autoimmune disease; cancer; bcl-w.  
XX  
OS Unidentified.  
XX  
US6221615-B1.  
XX  
PD 24-APR-2001.  
XX  
PF 25-JAN-1999; 99US-00236385.  
XX  
PR 12-MAY-1995; 95US-00440391.  
XX  
PR 08-AUG-1997; 97US-0008597.  
XX  
(APOP-) APOPTOSIS TECHNOLOGY INC.  
PI Chittenden TD, Lutz RJ;  
XX  
DR 2002-234950/29.  
XX  
WPI: Disclosure; Col 6; 37pp; English.

The present invention relates to novel peptides, designated GD domains, which are capable of modulating apoptosis. The GD domains are essential for Bak's interaction with Bcl-XL, and to Bak's cell killing function. The GD domains mediate key protein/protein interactions with multiple cell death regulatory molecules. Also described are methods of identifying agonists or antagonists of GD domains. The methods are useful for identifying agents capable of modulating GD domain mediated heterodimerisation or homodimerization. The methods are particularly useful in drug screening and design, e.g. for identifying agents for treating autoimmune disease or cancer, or for identifying modulators of apoptosis. The present sequence represents a peptide tested for it's ability to block GD domain-mediated interactions



SQ	Sequence 27 AA;	XX	ADD8350;
	Query Match 97.1%; Score 101; DB 3; Length 27;	AC	
	Best Local Similarity 95.0%; Pred. No. 2e-09; Mismatches 1; Indels 0; Gaps 0;	XX	XX
	Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	DT	09-SEP-2004 (first entry)
Qy	1 AADPLHEAMRAAGDEFETRF 20	XX	Derivative of human Bcl-w protein.
Db	4 AADPLHQAMRAAGDEFETRF 23	XX	Bcl-w; human; protein structure; protein co-ordinate data; mutant; KW mutant.
		XX	
	RESULT 4	OS	Homo sapiens.
	AAV36048 standard; protein; 168 AA.	OS	
ID	AAV36048	XX	Synthetic.
AC	AAV36048;	XX	
XX		XX	
DT	22-APR-1998 (first entry)	Key	Location/Qualifiers
XX		FT	Misc-difference 128
DE	Mouse bcl-w protein.	FT	/note= "wild-type Ala substituted by Glu"
XX	KW	XX	
	Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer; diagnosis; degenerative disease.	XX	
XX		PN	WO2004050697-A1.
OS	Mus sp.	XX	
PN	WO9735971-A1.	PD	17-JUN-2004.
XX		XX	
PD	02-OCT-1997.	PF	2003WO-AU001624.
XX		XX	
PP	27-MAR-1997; 97WO-AU000199.	PR	03-DEC-2002; 2002AU-00953259.
XX		XX	
PR	27-MAR-1996; 96AU-00008965.	PA	(HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX		XX	
PA	(ANRA-) ANRAD OPERATIONS PTY LTD.	PA	
XX		XX	
PI	Cory S, Adams JM, Gibson LM, Holmgreen SP;	PI	Claim 16; Page 805-806; 810PP; English.
XX		XX	
WPI:	1997-489635/45.	PS	The present invention relates to a solution comprising a molecule or
DR	N-PSDB; AAT96578.	XX	CC molecular complex that comprises at least a fragment of Bcl-w. Also
XX		CC	CC disclosed is the structure of Bcl-w, in the form of protein coordinate
PT		CC	CC data. The solution is useful for identifying, selecting or designing
PR		CC	CC agents that are capable of inhibiting or potentiating one or more
PR		CC	CC biological activity of Bcl-w, and in solving the structures of other
PA	(ANRA-) ANRAD OPERATIONS PTY LTD.	PT	CC proteins with similar structure. It is also useful for characterizing the
XX		XX	CC three-dimensional structure of the Bcl-w molecule, molecular complex or
PS		PS	CC its derivative. The present sequence is a derivative of the human Bcl-w
XX		XX	CC protein.
DR		SQ	Sequence 183 AA;
XX		XX	
WPI:	1997-489635/45.	Query	Match 97.1%; Score 101; DB 8; Length 183;
DR	N-PSDB; AAT96578.	Best Local Similarity 95.0%; Pred. No. 2e-08; Mismatches 1; Indels 0; Gaps 0;	
XX		Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
PT		Qy	1 AADPLHEAMRAAGDEFETRF 20
PR		Db	38 AADPLHQAMRAAGDEFETRF 57
PR			
XX		RESULT 6	
CC		ID	AAM97394
CC	This sequence represents a novel protein, bcl-w, encoded by the mouse bcl	AC	AAM97394 standard; protein; 192 AA.
CC	-2 gene family. This gene promotes cell survival, so its modulation is	XX	
CC	useful in treatment of cancer or auto-immune diseases, degenerative	AC	AAM97394;
CC	diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular	XX	
CC	degeneration, hypoxia, ischaemia, human immunodeficiency virus infection	DT	20-MAY-1999 (first entry)
CC	or in cell transplants. Up-regulation of the gene can also be used to	XX	
CC	modify cell lines cultured <i>in vivo</i> , e.g. to develop new lines, to	DE	Mammalian bcl-w protein.
CC	facilitate isolation of hybridomas and to increase survival of primary	XX	
CC	recombinant Bcl-w for therapy, diagnosis, antibody production or	XX	
CC	screening of potential modulators	XX	
XX	Sequence 168 AA;	XX	
Query Match 97.1%; Score 101; DB 2; Length 168;	Query Match 97.1%; Score 101; DB 8; Length 183;		
Best Local Similarity 95.0%; Pred. No. 1.8e-08; Mismatches 1; Indels 0; Gaps 0;	Best Local Similarity 95.0%; Pred. No. 2e-08; Mismatches 1; Indels 0; Gaps 0;		
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;		
Qy	1 AADPLHEAMRAAGDEFETRF 20	Qy	1 AADPLHEAMRAAGDEFETRF 20
Db	38 AADPLHQAMRAAGDEFETRF 57	Db	38 AADPLHQAMRAAGDEFETRF 57
RESULT 5			
ADP8350			
ID	ADP8350 standard; protein; 183 AA.		





SQ	Sequence 193 AA;	XX	The human bcl- $\gamma$ protein.
	Query Match 97.1%; Score 101; DB 2; Length 193;	XX	Rat bcl- $\gamma$ protein; Rbcl- $\gamma$ ; human bcl- $\gamma$ protein; Rbcl- $\gamma$ ; bcl-2 homologue;
	Best Local Similarity 95.0%; Pred. No. 2.1e-08; Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	XX	programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
	QY 1 AADPLHEAMRAAGDEFEFRF 20	XX	head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
Db	38 AADPLHQAMRAAGDEFEFRF 57	XX	multiple sclerosis; myocardial infarction; vitally induced cell death;
		XX	aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
		XX	premature cell death; cell death stimulator; prolonged cell life span;
		XX	Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.
	RESULT 11	OS Homo sapiens.	
	AAW61391 standard; protein; 193 AA.	XX	
ID	AAW61391;	PN US5883229-A.	
XX		XX	
AC		PD 16-MAR-1999.	
XX		XX	
DT	02-OCT-1998 (first entry)	PF 25-NOV-1997;	97US-00978523.
XX		XX	
DE	Rat bcl- $\gamma$ protein.	PR 23-FEB-1996;	96US-0012201P.
XX		PR 11-FEB-1997;	97US-00798597.
XX	bcl- $\gamma$ ; bcl-2; cell death pathway; apoptotic; apoptosis; rat.	XX	
OS	Rattus sp.	PA (COCE-) COCENSYN INC.	
XX		XX	
PN	US5789201-A.	PI Guastella J;	
XX		XX	
PD	04-AUG-1998.	PS 1999-214150/18.	
XX		DR N-PSDB; AAX15946.	
PF	11-FEB-1997;	XX	
XX	97US-00798897.	PT Novel bcl- $\gamma$ homologues of the rat and human bcl-2 protein - useful for modulating programmed cell death.	
PR	23-FEB-1996;	XX	
XX	96US-0012201P.	PS Claim 1; Col 17-18; 26pp; English.	
PA	(COCE-) COCENSYN INC.	XX	
XX		CC The present sequence represents human bcl- $\gamma$ protein (Rbcl- $\gamma$ ). The specification also describes rat bcl- $\gamma$ protein (Rbcl- $\gamma$ ). Rbcl- $\gamma$ and Rbcl- $\gamma$ are homologues of the bcl-2 protein thought to be involved in programmed cell death (apoptosis and necrosis). Rbcl- $\gamma$ and Rbcl- $\gamma$ proteins may be used to treat conditions associated with a disruption of the cell death pathway. If they act as cell death inhibitors, they may be used in therapies to treat subjects suffering from: strokes, head trauma, Alzheimer's Disease, neural and muscular degenerative diseases (especially multiple sclerosis), myocardial infarction, vitally induced cell death, aging, spinal cord injuries and ankyrotrophic lateral sclerosis - conditions where cells under go premature cell death as a result of triggers which may or may not be apparent. They may also be used in this period to develop cell lines which remain viable in culture for an extended period. In contrast, if they act as cell death stimulators, Rbcl- $\gamma$ and Rbcl- $\gamma$ may be used to treat conditions associated with prolonged cell life span such as cancer (especially kaposi's sarcoma and lung cancer) and auto/hyperimmune diseases. They may also be used to cause cell death in, and hence control, parasites	
PI	Guastella J;	XX	
XX		CC Sequence 193 AA;	
DR	WPI; 1998-446079/38.	Query Match 97.1%; Score 101; DB 2; Length 193;	
XX	N-PSDB; AAV2333.	Best Local Similarity 95.0%; Pred. No. 2.1e-08; Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
PT	Nucleic acids encoding B-cell lymphoma- $\gamma$ protein - useful for producing recombinant protein for use in treating uncontrolled cell growth e.g. cancers.	Qy 1 AADPLHEAMRAAGDEFEFRF 20	
PR	Example: Fig 3A; 27pp; English.	Db 38 AADPLHQAMRAAGDEFEFRF 57	
XX	The mammalian bcl- $\gamma$ protein is a member of the bcl-2 family, components in the cell death pathway. The bcl-2 family have both apoptotic activity and the apoptosis blocking activity. bcl- $\gamma$ falls in the apoptosis activity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to recombinant genetic constructs to increase its expression in vivo. Also, antisense constructs can be used in disorders where prevention of cell death is desired.	RRSLT 1.3	
SQ	Sequence 193 AA;	XX	AAW97391
	Query Match 97.1%; Score 101; DB 2; Length 193;	XX	AAW97391 standard; protein; 193 AA.
	Best Local Similarity 95.0%; Pred. No. 2.1e-08; Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	AC AAW97391;	
QY	1 AADPLHEAMRAAGDEFEFRF 20	XX	20-MAY-1999 (first entry)
Db	38 AADPLHQAMRAAGDEFEFRF 57	AC AAW97391;	
		XX	The rat bcl- $\gamma$ protein.

Rat bcl- $\gamma$  protein; Rbcl- $\gamma$ ; human bcl- $\gamma$  protein; Rbcl- $\gamma$ ; bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.

Rattus sp.

US5883229-A.

16-MAR-1999.

25-NOV-1997; 97US-00978523.

23-FEB-1996; 96US-0012201P.

11-FEB-1997; 97US-00798857.

(COCE-) COCENSYN INC.

Guastella J;

WPI: 1999-214150/18.

DR N-PSDB; AAX15945.

Novel bcl- $\gamma$  homologues of the rat and human bcl-2 protein - useful for modulating programmed cell death.

Disclosure; Col 15-18; 26pp; English.

The present sequence represents rat bcl- $\gamma$  protein (Rbcl- $\gamma$ ). The specification also describes human bcl- $\gamma$  protein (Hbcl- $\gamma$ ). Rbcl- $\gamma$  and Hbcl- $\gamma$  are homologues of the bcl-2 protein thought to be involved in programmed cell death (apoptosis and necrosis). Rbcl- $\gamma$  and Hbcl- $\gamma$  proteins may be used to treat conditions associated with a disruption of the cell death pathway. If they act as cell death inhibitors, they may be used in therapies to treat subjects suffering from: strokes, head trauma, Alzheimer's Disease, neural and muscular degenerative diseases (especially multiple sclerosis), myocardial infarction, vitally induced cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis - conditions where cells undergo premature cell death as a result of triggers which may or may not be apparent. They may also be used in this way to develop cell lines which remain viable in culture for an extended period. In contrast, if they act as cell death stimulators, Rbcl- $\gamma$  and Hbcl- $\gamma$  may be used to treat conditions associated with prolonged cell life span such as cancer (especially kaposi's sarcoma and lung cancer) and hence control metastases. They may also be used to cause cell death in and hence control

KW	animal model.
XX	
OS	Homo sapiens.
XX	
PN	WO913710-A1.
XX	
PD	25-MAR-1999.
XX	
PF	16-SEP-1998;
XX	98WO-AU000764.
PR	16-SEP-1997;
XX	97AU-00009228.
PA	(HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX	
PI	Cory S, Adams J, Print C, Gibson L, Koentgen F;
XX	
DR	WPI; 1999-243390/20.
DR	N-B5DB; AAX25132.
XX	
PT	An animal model exhibiting reduced levels of a Bcl-w protein and/or
PT	protein associated with Bcl-w.
XX	
PS	Claim 2: Page 33; 52pp; English.
XX	
CC	The present sequence is human Bcl-w, a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for
CC	spermatogenesis. The invention relates generally to a method of treatment
CC	and to an animal model for the identification of molecules and genetic
CC	sequences useful for inducing or reducing fertility of male animals.
CC	Methods are provided for the treatment of infertility, or for reducing
CC	fertility, by modulating spermatogenesis. An animal model carries a
CC	mutation at least one allele of the human or murine bcl-w gene (see
CC	AAX25132-35) or in a gene associated with bcl-w. Such animals have
CC	disorganised seminiferous tubules and are substantially infertile, but
CC	possess no other major abnormalities as determined by histological
CC	examination. They can be used to screen for therapeutic molecules
CC	including genetic sequences capable of inducing, enhancing or otherwise
CC	facilitating spermatogenesis in animals, or which can induce infertility
XX	
Sequence	Sequence 193 AA;
SQ	
Qy	Query Match 97.1%; Score 101; DB 2; Length 193;
Db	Best Local Similarity 95.0%; Pred. No. 2.1e-08;
	Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0
Qy	1 AADPHHEAMBAAGDGFETR 20
Db	38 AADPHQAMRAAGDGFETR 57

PA (HALL-) HALL INST MEDICAL RES WALTER &amp; ELIZA.

XX Cory S, Adams J, Print C, Gibson L, Koentgen F;

PI DR 1999-243890/20.

XX N-PSDB; AAX5134.

PR An animal model exhibiting reduced levels of a Bcl-w protein and/or

PR protein associated with Bcl-w.

XX Disclosure; Page 37; 52pp; English.

XX The present sequence is described of a derivative of human Bcl-w (see also AY05530), a pro-survival member of the Bcl-2 family that is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bcl-w gene (see AAX25132-35) or in a gene associated with bcl-w. Such animals have disorganized seminiferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce infertility

XX SQ Sequence 193: AA;

Query Match	97.1%	Score 101;	DB 2;	Length 193;
Best Local Similarity	95.0%	Pred. No. 2.1e-08;		
Matches	19;	Conservative	1;	Mismatches 0;
				Indels 0;
				Gaps 0;

Qy 1 AADPLHEANRAAGDEFETRF 20  
Db 38 AADPLHQAMRAAGDEFETRF 57

Search completed: January 25, 2005, 10:14:37  
Job time : 119.5 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

M protein - protein search, using sw model

run on: January 25, 2005, 10:06:01 ; Search time 132 Seconds  
(without alignments)  
87.178 Million cell updates/sec

title: US-09-828-870-39  
parent score: 104  
sequence: 1 AADPLHEAMRAAGDEFETRF 20

Scoring Table: BIOSIM62

Gapop 10.0 , Gapext 0.5

searched: 1825181 8888 675374646 ~~2001-2006~~

total number of hits satisfying chosen parameters: 1825181

minimum DB seq length: 0

boost-processing: Minimum Match 0%

Maximum Match 100% Command

卷之三

```
database := UniProt_02;*
```

תְּנַשְּׁאָלָה בְּבָשָׂר וְבָשָׂר בְּתְּנַשְּׁאָלָה

greater than or equal to the score of the total score distribution.

200

Score	Query No.	Match	Length	DB	ID	Description	
						Start	End
1	101	97.1	178	2	Q8cfr2	mus musculu	Q8cfr2
2	101	97.1	178	2	Q9c1w5	mus musculu	Q9c1w5
3	101	97.1	193	1	Bc1w_hUMAN	homo sapien	Q92843
4	101	97.1	193	1	Bc1w_MOUSE	mus musculu	P70345
5	101	97.1	193	2	Q89966	rattus norvegicus	Q89966
6	101	97.1	193	2	Bab23468	mus musculu	Bab23468
7	101	97.1	219	2	Q7t560	rattus norvegicus	Q7t560
8	92	88.5	193	2	Q8cgl4	mus musculu	Q8cgl4
9	73	70.2	188	2	Q6cp82	xenopus laevis	Q6cp82
10	73	70.2	228	1	Ar1_xenla	xenopus laevis	Q91827
11	54	51.9	89	2	Q8t0w1	gallus gallus	Q8t0w1
12	54	51.9	229	1	Bc1x_chick	gallus gallus	Q07816
13	51	49.0	125	2	Q9h1r5	homo sapien	Q9h1r5
14	51	49.0	170	2	Q9rdt5	rattus norvegicus	Q9rdt5
15	51	49.0	170	2	Aaf81262	rattus norvegicus	Aaf81262
16	51	49.0	180	2	Q9bdd5	bos taurus	Q9bdd5
17	51	49.0	180	2	Q9dpx7	bos taurus	Q9dpx7
18	51	49.0	188	2	Q9h1r6	homo sapien	Q9h1r6
19	51	49.0	188	2	Q9ewx2	mus musculu	Q9ewx2
20	51	49.0	217	2	Q9n35	mus musculu	Q9n35
21	51	49.0	219	2	Q9nn36	mus musculu	Q9nn36
22	51	49.0	233	1	Bc1x_hUMAN	homo sapien	Q07817
23	51	49.0	233	1	Bc1x_MOUSE	mus musculu	Q64373
24	51	49.0	233	1	Bc1x_PIG	sus scrofa	Q573563
25	51	49.0	233	1	Bc1x_RAT	rattus norvegicus	Q761t7
26	51	49.0	233	2	Q761t7	canis familiaris	Q761t7
27	51	49.0	233	2	Q9nyw4	oryctolagus cuniculus	Q9nyw4
28	51	49.0	233	2	Q9n2s7	ovis aries	Q9n2s7
29	51	49.0	233	2	Q9n1a2	sus scrofa	Q9n1a2
30	51	49.0	233	2	Q8s942	felis silvestris	Q8s942
31	51	49.0	233	2	Bab71819	canis familiaris	Bab71819

51	49.0	233	2	APP35872	homo sapi
51	49.0	233	2	O35843	mus musculus
51	49.0	284	2	Q7TS62	rattus norvegicus
50	48.1	233	1	BCL2	CHICK
49	47.1	610	2	Q9T781	pseudomonas
37	46.2	179	2	Q5YWH2	oryza sativa
38	46.2	179	2	BAD16383	oryza sativa
48	46.2	325	2	Q73WB6	mycobacterium
48	46.2	325	2	AAB05091	mycobacterium
48	46.2	942	2	Q82EJ4	streptomyces
48	46.2	952	1	Q9x909	streptomyces
48	46.2	1788	2	Q8LG61	caenorhabditis
47	45.2	47	2	Q9YK2	arabidopsis
47	45.2	452	2	Q6DTP3	erwinia carotovora
				Q6DTP3	erwinia carotovora

## ASSIGNMENTS

RESULT 1	Q8CFR2	PRELIMINARY;	PRT;	178 AA.
Q8CFR2	Q8CFR2;			
ID	Q8CFR2;			
AC	Q8CFR2;			
DT	01-MAR-2003	(TREMBLrel. 23; Created)		
DT	01-MAR-2003	(TREMBLrel. 23; Last sequence update)		
DT	01-OCT-2003	(TREMBLrel. 25; Last annotation update)		
DE	BC1212_protein.			
GN	Name=BC1212;			
OS	Mus musculus (Mouse).			
OC	Karyotype; Metazoa; Chordata; Craniata; Vertebrata;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Eye;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Stramberg P.L., Feingold E.A., Grouse L.H., Derge			
RA	Klausner R.D., Collins F.S., Wagner L., Sheppard C.M.			
RA	Altachul S.F., Zeeberg B.R., Buetow K.H., Schaefer J.			
RA	Magnusson R.F., Jonsson H.H., Moore T., Max S.I., Wang J.			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M.			
RA	Stapleton M., Soares M.B., Donaldson M.F., Casavant T.			
RA	Barlow M.J., Uedin T.B., Toshiyuki S., Carninci P.			
RA	Loquaiello N.A., Peters G.J., Abramson R.			
RA	Raha S.S., McEwan P.J., McKernan K.J., Malek J.A.			
RA	Bosak S.A., McEwan P.J., Hale S., Garcia A.M., Gay			
RA	Richards S., McEwan P.J., Hale S., Garcia A.M., Gay			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gu			
RA	Fahy J., Heelon A., Ketteman M., Madan A., Rodriguez			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bo			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson			
RA	Rodriguez A.C., Grimwade J., Schmutz J., Myers R.M.			
RA	Skalski M.I., Smailus D.E., Schnarch			
RA	Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000			
RT	and mouse cDNA sequences";			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
RN	[12]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Eye;			
RA	Strausberg R.L.			
RL	Submitted (Nov-2002) to the EMBL/GenBank/DBJ database			
DR	EMBL; BC040369; AAH40369.1; -.			
DR	HS3P; Q92843; 100L			
DR	MGI; MG1:1080512; Bc1212.			
DR	GO; GO:0005515; P:protein binding; IPI.			
DR	GO; GO:0001915; P:apoptosis; IDA.			
DR	InterPro; IPR000712; Bc12_BH.			
DR	InterPro; IPR003093; Bc12_BH4.			
DR	InterPro; IPR002475; Bc12_Family.			
DR	Pfam; PF00452; Bc1-2; 1.			
DR	Pfam; PF02180; BH4; 1.			
DR	SMART; SM00337; BCL1; 1.			
DR	SMART; SM00265; BH4; 1.			

51	49.0	233	2	APP35872	homo sapi
51	49.0	233	2	O35843	mus musculus
51	49.0	284	2	Q7TS62	rattus norvegicus
50	48.1	233	1	BCL2	CHICK
49	47.1	610	2	Q9T781	pseudomonas
37	46.2	179	2	Q5YWH2	oryza sativa
38	46.2	179	2	BAD16383	oryza sativa
48	46.2	325	2	Q73WB6	mycobacterium
48	46.2	325	2	AAB05091	mycobacterium
48	46.2	942	2	Q82EJ4	streptomyces
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48	46.2	1788	2	Q8LG61	caenorhabditis
47	45.2	47	2	Q9YK2	arabidopsis
47	45.2	47	2	Q6DTP3	erwinia carotovora
				Q6DTP3	erwinia carotovora

RESULT 1	Q8CFR2	PRELIMINARY;	PRT;	178 AA.
Q8CFR2	Q8CFR2;			
ID	Q8CFR2;			
AC	Q8CFR2;			
DT	01-MAR-2003	(TREMBLrel. 23; Created)		
DT	01-MAR-2003	(TREMBLrel. 23; Last sequence update)		
DT	01-OCT-2003	(TREMBLrel. 25; Last annotation update)		
DE	BC1212_protein.			
GN	Name=BC1212;			
OS	Mus musculus (Mouse).			
OC	Karyotype; Metazoa; Chordata; Craniata; Vertebrata;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Eye;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Stramberg R.L., Feingold E.A., Grouse L.H., Derge			
RA	Klausner R.D., Collins F.S., Wagner L., Sheppard C.M.			
RA	Altachul S.F., Zeeberg B.R., Buetow K.H., Schaefer J.			
RA	Magnus R.F., Jordan H.H., Moore T., Max S.I., Wang J.			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M.			
RA	Stapleton M., Soares M.B., Donaldson M.F., Casavant T.			
RA	Brabstein M.J., Uedin T.B., Toshiyuki S., Carninci P.			
RA	Loquaiello N.A., Peters G.J., Abramson R.			
RA	Raha S.S., McEwan P.J., McKernan K.J., Malek J.A.			
RA	Bosak S.A., McEwan P.J., Hale S., Garcia A.M., Gay			
RA	Richards S., McEwan P.J., Hale S., Garcia A.M., Gay			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gu			
RA	Fahy J., Heelon A., Ketteman M., Madan A., Rodriguez R.W., Touchman J.W., Green E.D., Dickson			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bo			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson			
RA	Rodriguez A.C., Grimwold J., Schmutz J., Myers R.M.			
RA	Skalska U., Smailus D.R., Schnerch			
RA	Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000			
RT	RT and mouse cDNA sequences";			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
RN	[12]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Eye;			
RA	Strausberg R.L.			
RL	Submitted (Nov-2002) to the EMBL/GenBank/DBJ database			
DR	EMBL; BC040369; AAH40369.1; -.			
DR	HS3P; Q92843; 100L			
DR	MGI; MG1:1080512; Bc1212.			
DR	GO; GO:0005515; P:protein binding; IPI.			
DR	GO; GO:0001915; P:apoptosis; IDA.			
DR	InterPro; IPR000712; Bc12_BH.			
DR	InterPro; IPR003093; Bc12_BH4.			
DR	InterPro; IPR002475; Bc12_Family.			
DR	Pfam; PF00452; Bc1-2; 1.			
DR	Pfam; PF02180; BH4; 1.			
DR	SMART; SM00337; BCL1; 1.			
DR	SMART; SM00265; BH4; 1.			







OX NCBI\_TaxID=10090;  
 RN [1] SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Lung;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA The FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 full-length cDNAs.";  
 RT 60,710 full-length cDNAs.;  
 RL Nature 420:563-573 (2002).;  
 RN [2] RPK FANTOM Consortium;  
 RP STRAIN=C57BL/6J; TISSUE=Lung;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA RIKEN FANTOM Consortium;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409: 685-690 (2001).;  
 RN [3] SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Lung;  
 RX MEDLINE=93279253; PubMed=10349636;  
 RA Carninci P., Hayashizaki Y.;  
 RA Carninci P., Hayashizaki Y., "High-efficiency full-length cDNA cloning.";  
 RL Meth. Enzymol. 303:19-44 (1999).;  
 RN [4] RPK FANTOM Consortium;  
 RC STRAIN=C57BL/6J; TISSUE=Lung;  
 RX MEDLINE=20499374; PubMed=11042159;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Konno H., Akiyama J., Nishi K., Kitaunai T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishihine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kasaiwagi K.,  
 RA Fujikawa S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuuwa S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 sequencing pipeline with 384 multicapillary sequencer.";  
 RL Genome Res. 10:1617-1630 (2000).;  
 RN [5] RPK FANTOM Consortium;  
 RC STRAIN=C57BL/6J; TISSUE=Lung;  
 RX MEDLINE=20530913; PubMed=11042159;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
 RA Konno H., Akiyama J., Nishi K., Kitaunai T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishihine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kasaiwagi K.,  
 RA Fujikawa S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuuwa S., Kawai J.,  
 RA Okazaki Y., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,  
 RA Matsuyama T., Okido T., Owa C., Saito R., Saito K., Sakai C.,  
 RA Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T.,  
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,  
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshihisa K., Yoshino M.,  
 RA Muramatsu M., Hayashizaki Y.;  
 RL Submitted (JNU-20001) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AK046680; BAB23468.1;  
 SQ SEQUENCE 193 AA; 20790 MW; 3662A185P5945DFB4 CRC64;

RESULT 7  
 Q7TS60 PRELIMINARY; PRT; 219 AA.  
 ID Q7TS60  
 AC  
 DT 01-OCT-2003 (TREMBLrel. 25, Created)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE BCL-WEL.  
 OS Rattus norvegicus (Rat).  
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Rattus.  
 OC NCBI\_TaxID=10116;  
 RN [1] RPK FANTOM Consortium;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley;  
 RX MEDLINE=2267518; PubMed=12787066;  
 RA Itoh T., Itoh A., Pleasure D.;  
 RT "Bcl-2-related protein family gene expression during oligodendroglial differentiation.";  
 RL J. Neurochem. 85:1500-1512 (2003).  
 DR EMBL; AY185100; AAO64470.1;  
 DR GO:0042981; P:regulation of apoptosis; IEA.  
 DR InterPro; IPR00712; Bcl2\_BH.  
 DR InterPro; IPR003093; Bcl2\_BH4.  
 DR InterPro; IPR02475; Bcl2\_Family.  
 DR Pfam; PF00452; Bcl2\_1.  
 DR Pfam; PF02180; BH4\_1.  
 DR SMART; SM00337; Bcl1.  
 DR SMART; SM00255; BH4\_1.  
 DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE; PS01080; BH1.  
 DR PROSITE; PS01258; BH2.  
 DR PROSITE; PS01260; BH4\_1.  
 DR PROSITE; PS50063; BH4\_1.  
 SQ SEQUENCE 219 AA; 23720 MW; 30E36041BC1DC66F CRC64;  
 Query Match 97.1%; Score 101; DB 2; Length 219;  
 Best Local Similarity 95.0%; Pred. No. 1.e-07;  
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 DR 1 AADPLHEAMRAAGDEFTRF 20  
 DR 64 AADPLHQAMRAAGDEFTRF 83

RESULT 8  
 Q8CGL4 PRELIMINARY; PRT; 193 AA.  
 ID Q8CGL4  
 AC  
 DT 01-MAR-2003 (TREMBLrel. 23, Created)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)  
 DE BC12-like protein 2.  
 GN Name=Bc12L2;  
 OS Mus musculus (Mouse).  
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC NCBI\_TaxID=1090;  
 RN [1] RPK FANTOM Consortium;  
 RP SEQUENCE FROM N.A.  
 RA Gilmour R.S.;  
 RA "Mouse keratinocytes express c98, a novel gene homologous to bcl-2,  
 RT that is stimulated by insulin-like growth factor 1 and prevents  
 RT dexamethasone-induced apoptosis";  
 RL Biochim. Biophys. Acta 1676:127-137 (2004).  
 DR HSSP; Q92843; 100L  
 DR MGI; MGI:108452; Bcl12L2.  
 DR GO: GO:0005515; P:protein binding; IPI.  
 DR GO: GO:0006915; P:apoptosis; IPI.

Query Match 97.1%; Score 101; DB 2; Length 193;  
 Best Local Similarity 95.0%; Pred. No. 1.e-07;  
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DR 1 AADPLHEAMRAAGDEFTRF 20  
 DR 38 AADPLHQAMRAAGDEFTRF 57

DR	InterPro; IPR00712; Bcl2 BH.
DR	InterPro; IPR00303; Bcl2 BH4.
DR	InterPro; IPR002475; BCL2_FAMILY.
PFam	PF00452; Bcl-2; 1.
PFam	PF02180; BH4; 1.
DR	SMART; SM00337; BCL; 1.
SMART	SM00265; BH4; 1.
DR	PROSITE; PS50062; BCL2_FAMILY; 1.
DR	PROSITE; PS01080; BH1; 1.
DR	PROSITE; PS01258; BH2; 1.
SQ	SEQUENCE 193 AA; 20958 MW; 60D7F9E4DC56DFAE CRC64;
Query Match	88.5%; Score 92; DB 2; Length 193;
Best Local Similarity	85.0%; Pred. No. 4.1e-06;
Matches	17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy	1 AADPLHEAMRAAGCDEFEFR 20
Db	38 AADPLHQAMRAAGCDELQTRF 57
RESULT 9	
Q6GP82	PRELIMINARY; PRT; 188 AA.
ID	Q6GP82; PRELIMINARY; PRT; 188 AA.
AC	Q6GP82; PRELIMINARY; PRT; 188 AA.
DT	05-JUL-2004 (TREMBLrel. 27, Created)
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE	Hypothetical protein.
OS	Xenopus laevis (African Clawed Frog)
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Xenopidae; Xenopus.
OC	NCBI_TaxID=8355;
OX	
RN	
RP	SEQUENCE FROM N.A.
RC	SEQUENCE-Spleen;
RX	MEDLINE=22388257; PubMed=12477932;
RA	Strasburger R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
RA	Hoffmann R.E., Jordan H., Moore T., Rubin G.M., Bhat N.K.,
RA	Diatchenko L., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
RA	Stapleton M.J., Marusina K., Farmer A.A., Rubin G.M., Bhat N.K.,
RA	Brownstein M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Schaefer C.F.,
RA	Raha S.S., Loquellano N.A., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Roskard S.A., McEwan P.J., Peters G.J., Abramson R.D., Mulilaty S.J.,
RA	Roskard S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Villanueva K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Fahy J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Sheehan Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimeswood J., Schmitz J., Myers R.M., Butterfield Y.S.,
RA	Krzywinski M.J., Skalska U., Smilis D.E., Schmerch A., Schein J.E.,
RA	Jones S.J., Marra M.A.,
RT	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences";
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN	
RP	SEQUENCE FROM N.A.
RC	SEQUENCE-Spleen;
RX	MEDLINE=22341132; PubMed=12454917;
RA	Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA	Richardson P.,
RT	"Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT	initiative";
RT	Dev. Dyn. 225:384-391 (2002).
RL	
RN	
RC	SEQUENCE FROM N.A.
RX	MEMLB; BC073259; AAH73259; -
DR	Submitted 04-Nov-2004 to the EMBL/GenBank/DBJ databases.
EMBL	BC073259; AAH73259; -
DR	FT DOMAIN 120 139 BH1.

T DOMAIN	171	186	BH2.
T TRANSMEM	207	227	Potential.
T SEQUENCE	228 AA;	25068 MW;	C499D49A585F8A9 CRC64;
Query Match Score	70.2%;	Score 73;	DB 1;
Best Local Similarity	75.0%;	Pred. No.	0.0044;
Matches	15;	Conservative	1;
Y 1 ADPLHEAMRAAGDEFEFR 20		Mismatches	4;
b 73 ASCALHSAMRAAGDFEFR 92		Indels	0;
Y 2 ADPLHEAMRAAGDEFEFR 20		Gaps	0;
Y 3 ASDVQALRAGDFEFLRY 21			
RESULT 11			
D Q8UWJ1 PRELIMINARY; PRT; 89 AA.			
C Q8UWJ1; 01-MAR-2002 (TREMBUREL. 20, Created)			
T 01-MAR-2002 (TREMBUREL. 20, Last sequence update)			
E 01-JUN-2003 (TREMBUREL. 24, Last annotation update)			
E Bcl-x (Fragment).			
S Gallus gallus (Chicken).			
C Archosauria; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Phasianidae; Phasianinae; Gallus.			
C NCBI_TaxID=9031;			
X [1] SEQUENCE FROM N.A.			
X TISSUE=Ovary;			
A Shi Z, Chagresan O.M., Williams J.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.			
R EMBL; AF032511; AAU35559; 1.			
R GO: GO:042981: P: regulation of apoptosis; IEA.			
R InterPro; IPR000712; Bcl2_BH.			
R InterPro; IPR002474; Bcl12_BH.			
R SMART; SM00337; BCL12_FAMILY.			
R PROSITE; PS01080; BH1; 1.			
R PROSITE; PS01159; BH3; 1.			
R NON_TER 1 1			
T NON_TER 89 89			
Q SEQUENCE 89 AA;	10124 MW;	B5B0BBE5F323A8C4 CRC64;	
Y 1 ADPLHEAMRAAGDEFEFR 20			
b 2 ADPLHEAMRAAGDEFEFR 20			
Y 3 ASDVQALRAGDFEFLRY 21			
RESULT 12			
D BCLX CHICK STANDARD; PRT; 229 AA.			
C 007916; Q98908; 01-PBB-1995 (Rel. 31, Created)			
T 01-NOV-1997 (Rel. 39, Last sequence update)			
E 05-ULI-2004 (Rel. 44, Last annotation update)			
E Apoptosis regulator Bcl1-X (Bcl-2-like 1 protein).			
N Name=BCLX; Synonyms=BCLX, BCL-X;			
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Phasianidae; Phasianinae; Gallus.			
C NCBI_TaxID=9031;			
X [1] SEQUENCE FROM N.A. (ISOFORM SHORT).			
X MEDLINE=3364977; PubMed=835789;			
A Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,			
A Turka L.A., Mao X., Nunez G., Thompson C.B.,			
A "bcl-x, a bcl-2-related gene that functions as a dominant regulator of			
P SEQUENCE FROM N.A. (ISOFORM LONG).			
P STRAIN=tubbard; White Mountain; TISSUE=Testis;			
R RP SEQUENCE FROM N.A. (ISOFORM LONG).			
R RC STRAIN=tubbard; White Mountain; TISSUE=Testis;			
R RX MEDLINE=9724485; PubMed=910311;			
R RA Vilagrassa X., Mequita C., Mequita J.;			
R RT "differentiation, expression of bcl-2 and bcl-x during chicken spermatogenesis".			
R RT "FUNCTION: Dominant regulator of apoptotic cell death. The short form displays cell death repressor activity, whereas the long isoform promotes apoptosis (By similarity)."			
R RL "SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear envelope (By similarity)."			
R CC "ALTERNATIVE PRODUCTS:			
R CC "Event=Alternative splicing; Named isoforms=2; Name=Long; IsoId=007816-1; Sequence=Displayed; Name=Short; IsoId=007816-2; Sequence=VSP_000514;"			
R CC "TISSUE SPECIFICITY: Highest expression in organs with lymphoid development.			
R CC "DOMAIN: BH4 domain seems to be involved in the anti-apoptotic function. Intract BH1 and BH2 domains are required for anti-apoptotic activity (By similarity)."			
R CC "SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.			
R CC "SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.			
R CC "SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.			
R CC "SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.			
R CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).			
R DR EMBL; 223110; CA80657; 1; DR EMBL; U26645; AA80657; 1; DR PIR; A47537; A47537.			
R DR HSSP; P53563; 1AF3.			
R DR InterPro; IPR000712; Bcl2_BH.			
R DR InterPro; IPR003043; Bcl2_BH4.			
R DR InterPro; IPR002475; BCL2_FAMILY.			
R DR InterPro; IPR00425; Bcl2_Reg.			
R DR Pfam; PF00452; Bcl12; 1.			
R DR Pfam; PF02180; BH4; 1.			
R DR TIGR00865; TIGR00865; BCL2_FAMILY; 1.			
R DR PROSITE; PS50062; BCL2_FAMILY; 1.			
R DR PROSITE; PS01080; BH1; 1.			
R DR PROSITE; PS01258; BH2; 1.			
R DR PROSITE; PS01259; BH3; 1.			
R DR PROSITE; PS01260; BH4; 1; 1.			
R DR PROSITE; PS50063; BH4; 1; 1.			
R KW Alternative splicing; Apoptosis; Transmembrane.			
F DOMAIN 4 24			
F DOMAIN 82 96			
F DOMAIN 125 144			
F DOMAIN 176 191			
F TRANSMEM 206 223			
F VARSPLIC 185 229			
F LSPK -> VRTALP (in isoform Short).			
F SQ SEQUENCE 229 AA;	25733 MW;	A97D3AA5D04C0E9DA CRC64;	
P Query Match 51.9%; Score 54; DB 1; Length 229;			
P Best Local Similarity 52.6%; Pred. No. 4;			
P Matches 10; Conservative 4; Mismatches 5; Indels 0; Gaps 0;			
P /FID=VSP_000514.			
P SQ SEQUENCE 229 AA;	25733 MW;	A97D3AA5D04C0E9DA CRC64;	
P Query Match 51.9%; Score 54; DB 1; Length 229;			
P Best Local Similarity 52.6%; Pred. No. 4;			
P Matches 10; Conservative 4; Mismatches 5; Indels 0; Gaps 0;			
P /FID=VSP_000514.			
P SQ SEQUENCE 229 AA;	25733 MW;	A97D3AA5D04C0E9DA CRC64;	
P Query Match 51.9%; Score 54; DB 1; Length 229;			
P Best Local Similarity 52.6%; Pred. No. 4;			
P Matches 10; Conservative 4; Mismatches 5; Indels 0; Gaps 0;			
P /FID=VSP_000514.			

DR :|:|:|:|:|:|: 79 ASDVRLDAGDEFELRY 97

RESULT 13

Q9H1R5 PRELIMINARY; PRT; 125 AA.

ID Q9H1R5; AC 1; DT 01-MAR-2001 (TREMBLrel. 16, Created) 01-MAR-2001 (TREMBLrel. 16, Last sequence update) DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update) DE BA24J16\_1.2 (BCL2-like 1 (Isoform 2)) (Fragment). GN Name=BCL2L1; OS Homo sapiens (Human); OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo; OX NCBI\_TAXID=9606; RN [1] - SEQUENCE FROM N.A.

RA Brown A.; RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases. EMBL; ALI60175; CAC1.0004.1; -. HSSP; Q07817; 1LXII. GO; GO:0042981; P:regulation of apoptosis; IEA. InterPro; IPR00712; Bcl2\_BH. InterPro; IPR003093; Bcl2\_BH4. InterPro; IPR00415; BCL2\_Family. PFam; PF00452; Bcl-2; 1. DR PF02180; BH4; 1. SMART; SM00265; BH4; 1. PROSITE; PS50062; BCL2\_FAMILY; 1. DR PROSITE; PS01259; BH3; 1. PROSITE; PS01260; BH4; 1; 1. PROSITE; PS50063; BH4; 1. FT 125. SQ SEQUENCE 125 AA; 13874 MW; D84C030651475365 CRC64;

Query Match 49.0%; Score 51; DB 2; Length 125; Best Local Similarity 64.3%; Pred. No. 6.5; Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0; Gaps 0;

Qy :|:|:|:|:|:|: 7 EAMRAAGDEFETRF 20 Db 88 QALREAGDEFELRY 101

RESULT 14

Q9NU15 PRELIMINARY; PRT; 170 AA.

ID Q9NU15; AC 1; DT 01-NOV-1999 (TREMBLrel. 12, Created) 01-NOV-1999 (TREMBLrel. 12, Last sequence update) DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update) DE Bcl-x short. OS Rattus norvegicus (Rat). OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Rattus. OX NCBI\_TAXID=10116; RN [1] - SEQUENCE FROM N.A.

RP SEQUENCE=Sprague-Dawley; TISSUE=cerebellum; RC STRAIN=Sprague-Dawley; TISSUE=cerebellum; RA Cao G.; Chen J.; Chen D.; DR Submitted (JUN 2000) to the EMBL/GenBank/DBJ databases. EMBL; AF27286; AF081262.1; -. DR AF27286; AF081262.1; -. SQ SEQUENCE 170 AA; 18987 MW; D90868EC7F69ED59 CRC64;

Query Match 49.0%; Score 51; DB 2; Length 170; Best Local Similarity 64.3%; Pred. No. 8.8; Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0; Gaps 0;

Qy :|:|:|:|:|:|: 7 EAMRAAGDEFETRF 20 Db 88 QALREAGDEFELRY 101

Search completed: January 25, 2005, 10:10:35  
Job time : 134 secs

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OM protein - protein search, using sw model

Run on: January 25, 2005, 10:05:02 ; Search time 24.5 Seconds  
(without alignments)  
78.544 Million cell updates/sec

Title: US-09-828-870-39

Perfect score: 104

Sequence: 1 AADPLHEAMRAGDEFETRF 20

Scoring table: BLOSUM62

Gapop: 10.0 , Gapext: 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing First 45 summaries

Database : PIR 79:\*

1: Pir1:\*

2: Pir2:\*

3: Pir3:\*

4: Pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	54	51.9	190	2	A47537		apoptosis regulator
2	53.5	51.4	232	2	S24390		transforming prote
3	51	49.0	170	2	I49055		bcl-x short - mouse
4	51	49.0	176	2	I67435		gene bcl-xshort pr
5	51	49.0	214	2	I49057		bcl-x transmembran
6	51	49.0	227	2	JE0203		apoptosis regulato
7	51	49.0	233	2	B47537		bcl-x long - mouse
8	51	49.0	233	2	I49056		BCL-X protein - ra
9	51	49.0	233	2	S51761		BCL-X-Long - rat
10	51	49.0	233	2	I67431		transforming prote
11	50	48.1	216	2	B37332		probable glutamine
12	50	48.1	233	2	A37332		probable DNA topoi
13	49	47.1	610	2	A83638		hypothetical prote
14	48	46.2	952	2	T36664		translocator prote
15	48	46.2	1788	2	T29043		type IV pilin biog
16	47	45.2	186	2	F86379		pyridoxine 4-oxida
17	47	45.2	205	1	TVHUB1		DNA topoisomerase
18	45	43.3	440	2	E70758		DNA topoisomerase
19	45	43.3	934	2	G70563		probable DNA topoi
20	45	43.3	947	2	H86933		transcription fact
21	45	43.3	1037	2	T13350		translocator prote
22	44	42.3	295	2	B86333		type IV pilin biog
23	44	42.3	408	2	A82078		pyridoxine 4-oxida
24	44	42.3	507	2	JC7855		DNA topoisomerase
25	44	42.3	596	1	WMBEH2		probable DNA topoi
26	44	42.3	866	2	C97365		hel10 protein u4905
27	44	42.3	881	2	AB2153		DNA topoisomerase
28	44	42.3	898	2	S74903		DNA topoisomerase
29	44	42.3	1021	2	G75403		DNA topoisomerase

## ALIGNMENTS

RESULT 1							
A47537	apoptosis regulator bcl-x - chicken						
C;Species: Gallus gallus (chicken)							
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004							
C;Accession: A47537							
R;Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.R.; Ding, L.; Lindsten, T.; Turka, L.A.; Cell 74, 597-608, 1993							
A;Title: bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptosis							
A;Reference number: PMID:93364979							
A;Accession: A47537							
A;Status: preliminary							
A;Molecule type: DNA							
A;Residues: 1-190 <BOI>							
A;Cross-references: UNIPROT:Q07816; GB:Z223110; GB:L20120; NID:9510898; PIDN:CAA80657.1; C;Superfamily: bcl apoptosis regulator, inhibitory type							
Query Match 51.9%; Score 54; DB 2; Length 190;							
Best Local Similarity 52.6%; Pred. No. 0.53; 4; Mismatches 5; Indels 0; Gaps 0;							
Db 79 ASDPRQLRDAGDFELRY 97							
RESULT 2							
S24390	transforming Protein (Bcl-2) homolog - chicken						
C;Species: Gallus gallus (chicken)							
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004							
C;Accession: S24390							
R;Cizals-Hatem, D.L.; Louie, D.C.; Tanaka, S.; Reed, J.C.							
Biochim. Biophys. Acta 1132, 109-113, 1992							
A;Title: Molecular cloning and DNA sequence analysis of cDNA encoding chicken homologue							
A;Reference number: PMID:92379084; PMID:1511008							
A;Accession: S24390							
A;Status: preliminary							
A;Molecule type: mRNA							
A;Cross-references: UNIPROT:Q000709; EMBL:Z11961; NID:962969; PIDN:CAA78018.1; PID:G6297							
C;Superfamily: bcl apoptosis regulator, inhibitory type							
C;Keywords: mitochondrion, transmembrane protein							
Query Match 51.4%; Score 53.5; DB 2; Length 232;							
Best Local Similarity 57.1%; Pred. No. 0.78; 3; Mismatches 5; Indels 1; Gaps 1;							
Db 81 AAPPGVHLRQAGDBFSRRY 101							

RESULT 3  
 I49055  
 bcl-x short - mouse  
 C;Species: *Mus musculus* (house mouse)  
 C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
 C;Accession: I49055  
 R;Pang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.  
 J. Immunol. 153, 438-4398, 1994  
 A;Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.  
 A;Reference number: I49055; MUID:95052604; PMID:7963517  
 A;Accession: I49055  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-170 <RES>  
 A;Cross-references: UNIPROT:Q64373; EMBL:U10100; NID:9506645; PIDN:AAA82172.1; PID:9506645  
 C;Genetics:  
 A;Gene: bcl-x  
 C;SuperFamily: bcl apoptosis regulator, inhibitory type  
 Query Match 49.0%; Score 51; DB 2; Length 170;  
 Best Local Similarity 64.3%; Pred. No. 1.4%;  
 Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 Qy 7 EAMRAAGDBEFTRF 20  
 :||:|||||:  
 Db 88 QALREAGDBEFELRY 101

RESULT 6  
 I674203  
 apoptosis regulator bcl-x isoform - human  
 N;Alternate names: h-bcl-xbeta  
 C;Species: *Homo sapiens* (man)  
 C;Date: 21-Aug-1998 #sequence\_revision 21-Aug-1998 #text\_change 09-Jul-2004  
 C;Accession: JB0203  
 R;Ban, J.; Eckhart, L.; Weninger, W.; Mildner, M.; Tschachler, E.  
 Biochem. Biophys. Res. Commun. 248, 147-152, 1998  
 A;Title: Identification of a human cDNA encoding a novel bcl-x isoform.  
 A;Reference number: JEB0203; MUID:98340865; PMID:9675101  
 A;Accession: JB0203  
 A;Molecule type: mRNA  
 A;Residues: 1-227 <BAN>  
 A;Cross-references: UNIPROT:Q07817; GB:U72398; NID:91622940; PIDN:AA817354.1; PID:91622940  
 C;Genetics:  
 A;Gene: bcl-x  
 A;Map Position: 20  
 C;SuperFamily: bcl apoptosis regulator, inhibitory type  
 Query Match 49.0%; Score 51; DB 2; Length 227;  
 Best Local Similarity 64.3%; Pred. No. 1.9%;  
 Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 Qy 7 EAMRAAGDBEFTRF 20  
 :||:|||||:  
 Db 88 QALREAGDBEFELRY 101

RESULT 7  
 B77537  
 apoptosis regulator bcl-xL - human  
 N;Alternate names: bcl-2-related protein  
 N;Contains: apoptosis regulator bcl-xS  
 C;Species: *Homo sapiens* (man)  
 C;Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 09-Jul-2004  
 C;Accession: B47537; C47537  
 R;Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Turk, L.A.;  
 Cell 74, 597-608, 1993  
 A;Title: Expression of members of the bcl-2 gene family in the immature rat ovary: equin  
 constitutive bcl-2 and bcl-xL messenger ribonucleic acid levels.  
 A;Reference number: I53295; MUID:95129487; PMID:7828536  
 A;Accession: I67435  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-176 <RES>  
 A;Cross-references: GB:S78284; NID:9998483; PIDN:AA860702.1; PID:9998483  
 C;Genetics:  
 A;Gene: bcl-x  
 C;SuperFamily: bcl apoptosis regulator, inhibitory type  
 Query Match 49.0%; Score 51; DB 2; Length 176;  
 Best Local Similarity 64.3%; Pred. No. 1.4%;  
 Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 Qy 7 EAMRAAGDBEFTRF 20  
 :||:|||||:  
 Db 94 QALREAGDBEFELRY 107

RESULT 5  
 I49057  
 bcl-x transmembrane deleted - mouse  
 C;Species: *Mus musculus* (house mouse)  
 C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
 C;Accession: I49057  
 R;Pang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.  
 J. Immunol. 153, 438-4398, 1994  
 A;Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.  
 A;Reference number: I49055; MUID:95052604; PMID:7963517  
 A;Accession: I49057  
 A;Molecule type: mRNA  
 A;Residues: 1-214 <RES>  
 A;Cross-references: UNIPROT:Q64373; EMBL:U10102; NID:9506649; PIDN:AAA82174.1; PID:9506649  
 Query Match 49.0%; Score 51; DB 2; Length 233;

Best Local Similarity 64.3%; Pred. No. 1.9;  
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0; Qy 7 EAMRAAGDEFETRF 20  
Db 88 QALREAGDEFELRY 101

RESULT 8  
I49056  
bcl-1 long - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I49056; S552866  
R;Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.  
J. Immunol. 153, 4388-4398, 1994  
A;Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.  
A;Reference number: 149055; MURID:95052604; PMID:963517  
A;Accession: I49056  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-233 <RES>  
A;Cross-references: UNIPROT:Q64373; EMBL:U10101; PIDN:9506647; PIDN:AAA82173.1; PID:95066  
R;Kameyama, H.; Michaud, G.Y.; Takatsu, K.; Okuma, M.  
Submitted to the EMBL Data Library, November 1994  
A;Description: IL-5 inhibits anti-IGM-induced apoptosis in an immature B cell line throu  
A;Reference number: S52866  
A;Accession: S52866  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-233 <KAM>  
A;Cross-references: EMBL:X83574; PIDN:9695622; PIDN:CAA58557.1; PID:9695623  
C;Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 49.0%; Score 51; DB 2; Length 233;  
Best Local Similarity 64.3%; Pred. No. 1.9;  
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0; Qy 7 EAMRAAGDEFETRF 20  
Db 88 QALREAGDEFELRY 101

RESULT 9  
S51761  
BCL-X protein - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 07-May-1995 #sequence\_revision 01-Sep-1995 #text\_change 09-Jul-2004  
C;Accession: S51761; S51762  
R;Michaelidis, T.M.  
Submitted to the EMBL Data Library, November 1994  
A;Reference number: S51761  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-233 <MIC>  
A;Cross-references: UNIPROT:PS3563; EMBL:X82537; PIDN:CAA57886.1; PID:9607176  
A;Experimental source: embryonic; brain  
A;Accession: S51762  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-125,189-233 <MT2>  
A;Cross-references: EMBL:X82537; PIDN:CAA57887.1; PID:9607176  
A;Experimental source: embryonic; brain  
A;Note: smaller form due to splicing  
C;Genetics:  
A;Introns: 125/3  
C;Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 49.0%; Score 51; DB 2; Length 233;  
Best Local Similarity 64.3%; Pred. No. 1.9;  
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0; Qy 7 EAMRAAGDEFETRF 20  
Db 88 QALREAGDEFELRY 101

RESULT 10  
I67431  
BCL-X-Long - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I67431  
R;Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.  
Endocrinology 136, 232-241, 1995  
A;Title: Expression of members of the bcl-2 gene family in the immature rat ovary: equi  
onstitutive bcl-2 and bcl-x long messenger ribonucleic acid levels.  
A;Reference number: I53295; PMID:7828536  
A;Accession: I67431  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-233 <RES>  
A;Cross-references: UNIPROT:PS3563; EMBL:U34963; PIDN:91004376; PMID:AAA77686.1;  
C;Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 49.0%; Score 51; DB 2; Length 233;  
Best Local Similarity 64.3%; Pred. No. 1.9;  
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0; Qy 7 EAMRAAGDEFETRF 20  
Db 88 QALREAGDEFELRY 101

RESULT 11  
B37332  
transforming protein (bcl-2-beta) - chicken  
C;Species: Gallus gallus (chicken)  
C;Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 28-Jul-2003  
C;Accession: B37332; S35452  
R;Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.  
Nucleic Acids Res 20, 4187-4192, 1992.  
A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a vari  
A;Reference number: A37332; PMID:92375724;  
A;Accession: B37332  
A;Molecule type: DNA  
A;Status: nucleic acid sequence not shown  
A;Residues: 1-216 <EGU>  
A;Cross-references: EMBL:D11381; EMBL:D11382  
C;Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 48.1%; Score 50; DB 2; Length 216;  
Best Local Similarity 56.2%; Pred. No. 2.3;  
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0; Qy 5 LHEMRAAGDEFETRF 20  
Db 87 VHLRQAGDEFESRY 102

RESULT 12  
A37332  
transforming protein (bcl-2-alpha) - chicken  
C;Species: Gallus gallus (chicken)  
C;Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 09-Jul-2004  
C;Accession: A37332; S35453  
R;Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.  
Nucleic Acids Res 20, 4187-4192, 1992.  
A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a vari  
A;Reference number: A37332; PMID:92375724;  
A;Accession: A37332  
A;Molecule type: DNA  
A;Status: nucleic acid sequence not shown  
A;Cross-references: UNIPROT:Q00709; EMBL:D11381

C;Genetics:  
 A;Intron: 189/3  
 C;Superfamily: bcl apoptosis regulator, inhibitory type  
 C;Keywords: mitochondrion; transforming protein; transmembrane protein

Query Match 48.1%; Score 50; DB 2; Length 233;  
 Best Local Similarity 56.2%; Pred. No. 2.7;  
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 QY 5 LHEAMRAAGDEFERF 20  
 DB 87 VHLALRQAGDEFERRY 102

RESULT 13  
 A83638  
 Probable glutamine amidotransferase PA0051 [imported] - *Pseudomonas aeruginosa* (strain B  
 C;Species: *Pseudomonas aeruginosa*  
 C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
 C;Accession: A83638  
 R:Shover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br  
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Foiger, K.R.; Kas, A.; Larbig, K.; Lim,  
 'Lory, S.; Olson, M.V.  
 Nature 406, 959-964, 2000  
 A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho  
 A;Accession: A83638  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-610 <STO>  
 A;Cross-references: UNIPROT:Q9I781; GB:AE004445; PMID:10934043  
 A;Experimental source: strain PA01  
 C;Genetics:  
 A;Gene: PA0051

Query Match 47.1%; Score 49; DB 2; Length 610;  
 Best Local Similarity 58.8%; Pred. No. 11;  
 Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
 QY 3 DPLHEAMRAAGDEFERF 19  
 DB 85 DALRERLRRAGHEFTR 101

RESULT 14  
 T36664  
 probable DNA topoisomerase I - *Streptomyces coelicolor*  
 C;Species: *Streptomyces coelicolor*  
 C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
 C;Accession: T36664  
 R:Seeger, K.J.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
 submitted to the EMBL Data Library, March 1999  
 A;Accession: T36664  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-952 <SEE>  
 A;Cross-references: UNIPROT:Q9X999; EMBL:AL035636; PIDN:CAB38480.1; GSPDB:GN00070; SCOBI  
 C;Genetics:  
 A;Gene: SCOEDB:SCH5\_06C  
 C;SuperFamily: bacterial type I DNA topoisomerase

Query Match 46.2%; Score 48; DB 2; Length 952;  
 Best Local Similarity 50.9%; Pred. No. 24;  
 Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;  
 QY 2 ADPLHEAMRAAGDEFERF 18  
 DB 377 AQEAEHAIRPSGDRFR 393

RESULT 15